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SEQUENCE LISTING

<110>  MENDEL BIOTECHNOLOGY, INC.
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<120>  PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS

<130>  MBI-0049CIP

<150>  09/810,836
<151>  2001-03-16

<150>  10/412,699
<151>  2003-04-10

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<151>  2002-06-14

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<151>  2003-02-25

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<160>  64

<170>  PatentIn version 3.2

<210>  1
<211>  1281
<212>  DNA
<213>  Arabidopsis thaliana

<220>
<223> G867 Predicted polypeptide sequence is paralogous to G9, G993, G1930

<400>  1
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taaatggaat cgagtagcgt tgatgagagt actacaagta caggttccat ctgtgaaacc     120

ccggcgataa ctccggcgaa aaagtcgtcg gtaggtaact tatacaggat gggaagcgga     180

tcaagcgttg tgttagattc agagaacggc gtagaagctg aatctaggaa gcttccgtcg     240

tcaaaataca aaggtgtggt gccacaacca aacggaagat ggggagctca gatttacgag     300

aaacaccagc gcgtgtggct cgggacattc aacgaagaag acgaagccgc tcgtgcctac     360

gacgtcgcgg ttcacaggtt ccgtcgccgt gacgccgtca caaatttcaa agacgtgaag     420

atggacgaag acgaggtcga tttcttgaat tctcattcga aatctgagat cgttgatatg     480

ttgaggaaac atacttataa cgaagagtta gagcagagta aacggcgtcg taatggtaac     540

ggaaacatga ctaggacgtt gttaacgtcg gggttgagta atgatggtgt ttctacgacg     600

gggtttagat cggcggaggc actgtttgag aaagcggtaa cgccaagcga cgttgggaag     660

ctaaaccgtt tggttatacc gaaacatcac gcagagaaac attttccgtt accgtcaagt     720

aacgtttccg tgaaaggagt gttgttgaac tttgaggacg ttaacgggaa agtgtggagg     780

ttccgttact cgtattggaa cagtagtcag agttatgttt tgactaaagg ttggagcagg     840

ttcgttaagg agaagaatct acgtgctggt gacgtggtta gtttcagtag atctaacggt     900

caggatcaac agttgtacat tgggtggaag tcgagatccg ggtcagattt agatgcgggt     960

cgggttttga gattgttcgg agttaacatt tcaccggaga gttcaagaaa cgacgtcgta    1020

ggaaacaaaa gagtgaacga tactgagatg ttatcgttgg tgtgtagcaa gaagcaacgc    1080
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atctttcacg cctcgtaaca actcttcttc tttttttttc ttttgttgtt ttaataattt    1140

ttaaaaactc cattttcgtt ttctttattt gcatcggttt ctttcttctt gtttaccaaa    1200

ggttcatgag ttgtttttgt tgtattgatg aactgtaaat tttatttata ggataaattt    1260

taaaaaaaaa aaaaaaaaaa a                                              1281


<210>  2
<211>  344
<212>  PRT
<213>  Arabidopsis thaliana

<220>
<223> G867 polypeptide Paralogous to G9, G993, G1930

<400>  2

Met Glu Ser Ser Ser Val Asp Glu Ser Thr Thr Ser Thr Gly Ser Ile
1               5                   10                  15


Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly Asn
            20                  25                  30


Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu Asn
        35                  40                  45


Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly
    50                  55                  60


Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65                  70                  75                  80


His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
                85                  90                  95


Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala Val
            100                 105                 110


Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe Leu
        115                 120                 125


Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr
    130                 135                 140


Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn Gly
145                 150                 155                 160


Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly Val
                165                 170                 175
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Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala Val
            180                 185                 190


Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His
        195                 200                 205


His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val Lys
    210                 215                 220


Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe
225                 230                 235                 240


Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
                245                 250                 255


Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val
            260                 265                 270


Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly Trp
        275                 280                 285


Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg Leu
    290                 295                 300


Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val Gly
305                 310                 315                 320


Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser Lys
                325                 330                 335


Lys Gln Arg Ile Phe His Ala Ser
            340


<210>  3
<211>  1246
<212>  DNA
<213>  Arabidopsis thaliana

<220>
<223> G9 Predicted polypeptide sequence is paralogous to G867, G993, G1930

<400>  3
gtgtttcttc tttctgctaa aaggttataa tttttgtttc ttggtttggt gagaatcttc      60

aagaaactga aacaaagaaa atggattcta gttgcataga cgagataagt tcctccactt     120

cagaatcttt ctccgccacc accgccaaga agctctctcc tcctcccgcg gcggcgttac     180

gcctctaccg gatgggaagc ggcgggagca gcgtcgtgtt ggatcccgag aacggcctag     240

agacggagtc acgaaagcta ccatcttcaa aatacaaagg tgttgttcct cagcctaacg     300
```

gaagatgggg agctcagatc tacgagaagc accaacgagt atggctcggg actttcaacg 360

agcaagaaga agctgctcgt tcctacgaca tcgcagcttg tagattccgt ggccgcgacg 420

ccgtcgtcaa cttcaagaac gttctggaag acggcgattt agcttttctt gaagctcact 480

caaaggccga gatcgtcgac atgttgagaa aacacactta cgccgacgag cttgaacaga 540

acaataaacg gcagttgttt ctctccgtcg acgctaacgg aaaacgtaac ggatcgagta 600

ctactcaaaa cgacaaagtt ttaaagacgt gtgaagttct tttcgagaag gctgttacac 660

ctagcgacgt tgggaagcta aaccgtctcg tgatacctaa acaacacgcc gagaaacact 720

ttccgttacc gtcaccgtca ccggcagtga ctaaaggagt tttgatcaac ttcgaagacg 780

ttaacggtaa agtgtggagg ttccgttact catactggaa cagtagtcaa agttacgtgt 840

tgaccaaggg atggagtcga ttcgtcaagg agaagaatct tcgagccggt gatgttgtta 900

ctttcgagag atcgaccgga ctagagcggc agttatatat tgattggaaa gttcggtctg 960

gtccgagaga aaacccggtt caggtggtgg ttcggctttt cggagttgat atctttaatg 1020

tgaccaccgt gaagccaaac gacgtcgtgg ccgtttgcgg tggaaagaga tctcgagatg 1080

ttgatgatat gtttgcgtta cggtgttcca agaagcaggc gataatcaat gctttgtgac 1140

atatttcctt ttccgatttt atgctttcgt tttttaattt ttttttttgt caagttgtgt 1200

aggttgtgat tcatgctagg ttgtatttag gaaaagagat aagacc 1246

<210> 4
<211> 352
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G9 polypeptide Paralogous to G867, G993, G1930

<400> 4

Met Asp Ser Ser Cys Ile Asp Glu Ile Ser Ser Ser Thr Ser Glu Ser
1 5 10 15

Phe Ser Ala Thr Thr Ala Lys Lys Leu Ser Pro Pro Pro Ala Ala Ala
20 25 30

Leu Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser Ser Val Val Leu Asp
35 40 45

Pro Glu Asn Gly Leu Glu Thr Glu Ser Arg Lys Leu Pro Ser Ser Lys
50 55 60

Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
65 70 75 80

```
Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Gln Glu
                85                  90                  95


Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys Arg Phe Arg Gly Arg
            100                 105                 110


Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu Asp Gly Asp Leu Ala
        115                 120                 125


Phe Leu Glu Ala His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys
    130                 135                 140


His Thr Tyr Ala Asp Glu Leu Glu Gln Asn Asn Lys Arg Gln Leu Phe
145                 150                 155                 160


Leu Ser Val Asp Ala Asn Gly Lys Arg Asn Gly Ser Ser Thr Thr Gln
                165                 170                 175


Asn Asp Lys Val Leu Lys Thr Cys Glu Val Leu Phe Glu Lys Ala Val
            180                 185                 190


Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
        195                 200                 205


His Ala Glu Lys His Phe Pro Leu Pro Ser Pro Ser Pro Ala Val Thr
    210                 215                 220


Lys Gly Val Leu Ile Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg
225                 230                 235                 240


Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
                245                 250                 255


Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val
            260                 265                 270


Val Thr Phe Glu Arg Ser Thr Gly Leu Glu Arg Gln Leu Tyr Ile Asp
        275                 280                 285


Trp Lys Val Arg Ser Gly Pro Arg Glu Asn Pro Val Gln Val Val Val
    290                 295                 300


Arg Leu Phe Gly Val Asp Ile Phe Asn Val Thr Thr Val Lys Pro Asn
305                 310                 315                 320


Asp Val Val Ala Val Cys Gly Gly Lys Arg Ser Arg Asp Val Asp Asp
                325                 330                 335
```

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Met Phe Ala Leu Arg Cys Ser Lys Lys Gln Ala Ile Ile Asn Ala Leu
            340                 345                 350


<210>  5
<211>  1239
<212>  DNA
<213>  Arabidopsis thaliana

<220>
<223> G993 Predicted polypeptide sequence is paralogous to G867, G9, G1930

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ctactactcc aaagccgaca acgacgacgg agaagaaact ctcttctccg ccggcgacgt     120

cgatgcgtct ctacagaatg ggaagcggcg gaagcagcgt cgttttggat tcagagaacg     180

gcgtcgagac cgagtcacgt aagcttcctt cgtcgaaata taaaggcgtt gtgcctcagc     240

ctaacggaag atggggagct cagatttacg agaagcatca gcgagtttgg ctcggtactt     300

tcaacgagga agaagaagct gcgtcttctt acgacatcgc cgtgaggaga ttccgcggcc     360

gcgacgccgt cactaacttc aaatctcaag ttgatggaaa cgacgccgaa tcggcttttc     420

ttgacgctca ttctaaagct gagatcgtgg atatgttgag gaaacacact tacgccgatg     480

agtttgagca gagtagacgg aagtttgtta acggcgacgg aaaacgctct gggttggaga     540

cggcgacgta cggaaacgac gctgttttga gagcgcgtga ggttttgttc gagaagactg     600

ttacgccgag cgacgtcggg aagctgaacc gtttagtgat accgaaacaa cacgcggaga     660

agcattttcc gttaccggcg atgacgacgg cgatggggat gaatccgtct ccgacgaaag     720

gcgttttgat taacttggaa gatagaacag ggaaagtgtg gcggttccgt tacagttact     780

ggaacagcag tcaaagttac gtgttgacca agggctggag ccggttcgtt aaagagaaga     840

atcttcgagc cggtgatgtg gtttgtttcg agagatcaac cggaccagac cggcaattgt     900

atatccactg gaaagtccgg tctagtccgg ttcagactgt ggttaggcta ttcggagtca     960

acattttcaa tgtgagtaac gagaaaccaa acgacgtcgc agtagagtgt gttggcaaga    1020

agagatctcg ggaagatgat ttgttttcgt tagggtgttc caagaagcag gcgattatca    1080

acatcttgtg acaaattctt tttttttggt tttttcttc aatttgtttc tcctttttca    1140

atattttgta ttgaaatgac aagttgtaaa ttaggacaag acaagaaaaa atgacaacta    1200

gacaaaatag tttttgttta aaaaaaaaaa aaaaaaaaa                           1239


<210>  6
<211>  361
<212>  PRT
<213>  Arabidopsis thaliana
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<220>
<223> G993 polypeptide Paralogous to G867, G9, G1930

<400>  6

Met Glu Tyr Ser Cys Val Asp Asp Ser Ser Thr Thr Ser Glu Ser Leu
1               5                   10                  15

Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys Leu
            20                  25                  30

Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser Gly
        35                  40                  45

Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu Ser
    50                  55                  60

Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn
65                  70                  75                  80

Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu
                85                  90                  95

Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile Ala
            100                 105                 110

Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser Gln
        115                 120                 125

Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser Lys
    130                 135                 140

Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe
145                 150                 155                 160

Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly
                165                 170                 175

Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu
            180                 185                 190

Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn
        195                 200                 205

Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro
    210                 215                 220

Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val
225                 230                 235                 240
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```
Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr
                245                 250                 255

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
            260                 265                 270

Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe
        275                 280                 285

Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val
    290                 295                 300

Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile
305                 310                 315                 320

Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val
                325                 330                 335

Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys Ser
            340                 345                 350

Lys Lys Gln Ala Ile Ile Asn Ile Leu
        355                 360


<210>  7
<211>  1155
<212>  DNA
<213>  Arabidopsis thaliana

<220>
<223> G1930 Predicted polypeptide sequence is paralogous to G867, G9, G993

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atttcgtttc ataacatgga tgccatgagt agcgtagacg agagctctac aactacagat     120

tccattccgg cgagaaagtc atcgtctccg gcgagtttac tatatagaat gggaagcgga     180

acaagcgtgg tacttgattc agagaacggt gtcgaagtcg aagtcgaagc cgaatcaaga     240

aagcttcctt cttcaagatt caaaggtgtt gttcctcaac caaatggaag atggggagct     300

cagatttacg agaaacatca acgcgtgtgg cttggtactt tcaacgagga agacgaagca     360

gctcgtgctt acgacgtcgc ggctcaccgt ttccgtggcc gcgatgccgt tactaatttc     420

aaagacacga cgttcgaaga agaggttgag ttcttaaacg cgcattcgaa atcagagatc     480

gtagatatgt tgagaaaaca cacttacaaa gaagagttag accaaaggaa acgtaaccgt     540

gacggtaacg gaaaagagac gacggcgttt gctttggctt cgatggtggt tatgacgggg     600
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tttaaaacgg cggagttact gtttgagaaa acggtaacgc caagtgacgt cgggaaacta     660

aaccgtttag ttataccaaa acaccaagcg gagaaacatt ttccgttacc gttaggtaat     720

aataacgtct ccgttaaagg tatgctgttg aatttcgaag acgttaacgg gaaagtgtgg     780

aggttccgtt actcttattg gaatagtagt caaagttatg tgttgaccaa aggttggagt     840

agattcgtta aagagaagag actttgtgct ggtgatttga tcagttttaa aagatccaac     900

gatcaagatc aaaaattctt tatcgggtgg aaatcgaaat ccgggttgga tctagagacg     960

ggtcgggtta tgagattgtt tggggttgat atttctttaa acgccgtcgt tgtagtgaag    1020

gaaacaacgg aggtgttaat gtcgtcgtta aggtgtaaga agcaacgagt tttgtaataa    1080

caatttaaca acttgggaaa gaaaaaaaag ctttttgatt ttaatttctc ttcaacgtta    1140

atcttgctga gatta                                                     1155


<210>  8
<211>  333
<212>  PRT
<213>  Arabidopsis thaliana

<220>
<223> G1930 polypeptide Paralogous to G867, G9, G993

<400>  8

Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr Thr Thr Asp Ser
1               5                   10                  15


Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met
            20                  25                  30


Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val
        35                  40                  45


Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly
    50                  55                  60


Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65                  70                  75                  80


His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
                85                  90                  95


Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val
            100                 105                 110


Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn
        115                 120                 125
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```
Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
    130                 135                 140

Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys
145                 150                 155                 160

Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe
                165                 170                 175

Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val
            180                 185                 190

Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His
        195                 200                 205

Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu
    210                 215                 220

Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser
225                 230                 235                 240

Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg
                245                 250                 255

Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys
            260                 265                 270

Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys
        275                 280                 285

Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val
    290                 295                 300

Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu Thr Thr Glu Val
305                 310                 315                 320

Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val Leu
                325                 330


<210>  9
<211>  1194
<212>  DNA
<213>  Arabidopsis thaliana

<220>
<223> G2687

<400>  9
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acgcaaagac ggagacttca gtgtcttcag gttcaagcga ctctttcttg cctctcaaga     120

aacgcatgag acttgatgac gaaccagaaa acgccctagt ggtttcgtct tcaccaaaga     180

cggttgtggc ttctggcaat gtcaagtaca aaggagtcgt tcagcaacag aacggtcatt     240

ggggtgccca gatttacgca gaccacaaaa ggatttggct tggaactttc aaatccgctg     300

atgaagccgc cacggcttac gatagtgcat ctatcaaact ccgaagcttt gacgctaact     360

cgcaccggaa cttcccttgg tctacaatca ctctcaacga accagacttt caaaattgct     420

acacaacaga gactgtgttg aacatgatca gagacggttc gtaccaacac aaattcagag     480

attttctcag aatcagatct cagattgttg cgagtatcaa catcggggga ccaaaacaag     540

cccgaggaga agtgaatcaa gaatcagaca agtgtttttc ttgcacacag ctttttcaga     600

aggaattgac accgagcgat gtagggaaac taaataggct tgtgatacct aaaaagtatg     660

cagtgaagta tatgcctttc ataagcgctg atcaaagcga gaaagaagag ggtgaaatag     720

taggatctgt ggaagatgtg gaggttgtgt tttacgacag agcaatgaga caatggaagt     780

ttaggtattg ttactggaaa agtagccaga gctttgtctt caccagagga tggaatagtt     840

tcgtgaagga gaagaatctc aaggagaagg atgttattgc cttctacact tgcgatgtcc     900

cgaacaatgt gaagacatta gaaggtcaaa gaaagaactt cttgatgatc gatgttcatt     960

gcttttcaga caacggttcc gtggtagctg aggaagtaag tatgacggtt catgacagtt    1020

cagtgcaagt aaagaaaaca gaaaacttgg ttagctccat gttagaagat aaagaaacca    1080

aatcagagga gaacaaagga gggtttatgc tgtttggtgt aaggatcgaa tgtccttagg    1140

gaatttttct ttaaaagttt cttacttcaa ctagaacttg ttttacttgt acct          1194


<210>  10
<211>  363
<212>  PRT
<213>  Arabidopsis thaliana

<220>
<223> G2687 polypeptide

<400>  10

Met Asn Asn Ile Asp Asp Ala Lys Thr Glu Thr Ser Val Ser Ser Gly
1               5                   10                  15


Ser Ser Asp Ser Phe Leu Pro Leu Lys Lys Arg Met Arg Leu Asp Asp
            20                  25                  30


Glu Pro Glu Asn Ala Leu Val Val Ser Ser Ser Pro Lys Thr Val Val
        35                  40                  45


Ala Ser Gly Asn Val Lys Tyr Lys Gly Val Val Gln Gln Gln Asn Gly
    50                  55                  60
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His Trp Gly Ala Gln Ile Tyr Ala Asp His Lys Arg Ile Trp Leu Gly
65                  70                  75                  80

Thr Phe Lys Ser Ala Asp Glu Ala Ala Thr Ala Tyr Asp Ser Ala Ser
                85                  90                  95

Ile Lys Leu Arg Ser Phe Asp Ala Asn Ser His Arg Asn Phe Pro Trp
            100                 105                 110

Ser Thr Ile Thr Leu Asn Glu Pro Asp Phe Gln Asn Cys Tyr Thr Thr
        115                 120                 125

Glu Thr Val Leu Asn Met Ile Arg Asp Gly Ser Tyr Gln His Lys Phe
    130                 135                 140

Arg Asp Phe Leu Arg Ile Arg Ser Gln Ile Val Ala Ser Ile Asn Ile
145                 150                 155                 160

Gly Gly Pro Lys Gln Ala Arg Gly Glu Val Asn Gln Glu Ser Asp Lys
                165                 170                 175

Cys Phe Ser Cys Thr Gln Leu Phe Gln Lys Glu Leu Thr Pro Ser Asp
            180                 185                 190

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Lys Tyr Ala Val Lys
        195                 200                 205

Tyr Met Pro Phe Ile Ser Ala Asp Gln Ser Glu Lys Glu Glu Gly Glu
    210                 215                 220

Ile Val Gly Ser Val Glu Asp Val Glu Val Val Phe Tyr Asp Arg Ala
225                 230                 235                 240

Met Arg Gln Trp Lys Phe Arg Tyr Cys Tyr Trp Lys Ser Ser Gln Ser
                245                 250                 255

Phe Val Phe Thr Arg Gly Trp Asn Ser Phe Val Lys Glu Lys Asn Leu
            260                 265                 270

Lys Glu Lys Asp Val Ile Ala Phe Tyr Thr Cys Asp Val Pro Asn Asn
        275                 280                 285

Val Lys Thr Leu Glu Gly Gln Arg Lys Asn Phe Leu Met Ile Asp Val
    290                 295                 300

His Cys Phe Ser Asp Asn Gly Ser Val Val Ala Glu Glu Val Ser Met
```

305 310 315 320

Thr Val His Asp Ser Ser Val Gln Val Lys Lys Thr Glu Asn Leu Val
325 330 335

Ser Ser Met Leu Glu Asp Lys Glu Thr Lys Ser Glu Glu Asn Lys Gly
340 345 350

Gly Phe Met Leu Phe Gly Val Arg Ile Glu Cys
355 360

<210> 11
<211> 1216
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1957

<400> 11
caagaaccat ctcgtaaatc aagatttctc caaggaaaat cagataagtc ataatggatc 60

tatccctggc tccgacaaca acaacaagtt ccgaccaaga acaagacaga gaccaagaat 120

taacctccaa catcggagca agcagcagct ccggtcccag cggaaacaac aacaaccttc 180

cgatgatgat gattccacct ccggagaaag aacacatgtt cgacaaagtg gtaacaccaa 240

gcgacgtcgg aaaactcaac agactcgtga tccctaaaca acacgctgag aggtatttcc 300

ctctagactc ctcaaacaac caaaacggca cgcttttgaa cttccaagac agaaacggca 360

agatgtggag attccgttac tcgtattgga actctagcca gagctacgtt atgaccaaag 420

gatggagccg tttcgtcaaa gagaaaaagc tcgatgcagg agacattgtc tctttccaac 480

gaggcatcgg agatgagtca gaaagatcca aactttacat agattggagg catagacccg 540

acatgagcct cgttcaagca catcagtttg gtaattttgg tttcaatttc aatttcccga 600

ccacttctca atattccaac agatttcatc cattgccaga atataactcc gtcccgattc 660

accggggctt aaacatcgga aatcaccaac gttcctatta taacacccag cgtcaagagt 720

tcgtagggta tggttatggg aatttagctg gaaggtgtta ctacacggga tcaccgttgg 780

atcataggaa cattgttgga tcagagccgt tggttataga ctcagtccct gtggttcccg 840

ggagattaac tccggtgatg ttaccgccgc ttcctccgcc tccttctacg gcgggaaaga 900

gactaaggct ctttggggtg aatatggaat gtggcaatga ctataatcaa caagaagagt 960

catggttggt gccacgtggc gaaattggtg catcttcttc ttcttcttca gctctacgac 1020

taaatttatc gactgatcat gatgatgata atgatgatgg tgatgatggc gatgatgatc 1080

aatttgctaa gaaagggaag tcttcacttt ctctcaattt caatccatga gaagtttcat 1140

catcttcttg ttttgaatct ctctttatat tgtttccatt agtaattttt actaagggta 1200

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ttagattcta gctagt                                                     1216


<210>  12
<211>  358
<212>  PRT
<213>  Arabidopsis thaliana

<220>
<223> G1957 polypeptide

<400>  12

Met Asp Leu Ser Leu Ala Pro Thr Thr Thr Thr Ser Ser Asp Gln Glu
1               5                   10                  15


Gln Asp Arg Asp Gln Glu Leu Thr Ser Asn Ile Gly Ala Ser Ser Ser
            20                  25                  30


Ser Gly Pro Ser Gly Asn Asn Asn Asn Leu Pro Met Met Met Ile Pro
        35                  40                  45


Pro Pro Glu Lys Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp
    50                  55                  60


Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg
65                  70                  75                  80


Tyr Phe Pro Leu Asp Ser Ser Asn Asn Gln Asn Gly Thr Leu Leu Asn
                85                  90                  95


Phe Gln Asp Arg Asn Gly Lys Met Trp Arg Phe Arg Tyr Ser Tyr Trp
            100                 105                 110


Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val
        115                 120                 125


Lys Glu Lys Lys Leu Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Gly
    130                 135                 140


Ile Gly Asp Glu Ser Glu Arg Ser Lys Leu Tyr Ile Asp Trp Arg His
145                 150                 155                 160


Arg Pro Asp Met Ser Leu Val Gln Ala His Gln Phe Gly Asn Phe Gly
                165                 170                 175


Phe Asn Phe Asn Phe Pro Thr Thr Ser Gln Tyr Ser Asn Arg Phe His
            180                 185                 190


Pro Leu Pro Glu Tyr Asn Ser Val Pro Ile His Arg Gly Leu Asn Ile
```

```
        195                 200                 205

Gly Asn His Gln Arg Ser Tyr Tyr Asn Thr Gln Arg Gln Glu Phe Val
    210                 215                 220

Gly Tyr Gly Tyr Gly Asn Leu Ala Gly Arg Cys Tyr Tyr Thr Gly Ser
225                 230                 235                 240

Pro Leu Asp His Arg Asn Ile Val Gly Ser Glu Pro Leu Val Ile Asp
                245                 250                 255

Ser Val Pro Val Val Pro Gly Arg Leu Thr Pro Val Met Leu Pro Pro
            260                 265                 270

Leu Pro Pro Pro Pro Ser Thr Ala Gly Lys Arg Leu Arg Leu Phe Gly
        275                 280                 285

Val Asn Met Glu Cys Gly Asn Asp Tyr Asn Gln Gln Glu Glu Ser Trp
    290                 295                 300

Leu Val Pro Arg Gly Glu Ile Gly Ala Ser Ser Ser Ser Ser Ser Ala
305                 310                 315                 320

Leu Arg Leu Asn Leu Ser Thr Asp His Asp Asp Asp Asn Asp Asp Gly
                325                 330                 335

Asp Asp Gly Asp Asp Asp Gln Phe Ala Lys Lys Gly Lys Ser Ser Leu
            340                 345                 350

Ser Leu Asn Phe Asn Pro
        355


<210>  13
<211>  1368
<212>  DNA
<213>  Arabidopsis thaliana

<220>
<223> G1010

<400>  13
attcttcttc taaaaaatct tgacaacttt ttgtttttgt tttctttctc tgaatttttt      60

aaaagagaga gagctatgta gctatgaaac agtaagagat atagatatag agagacagag     120

aaagatgatg atcagtgaag ttaggctaaa cccactttct atttatgtat aattaggtca     180

atcacatcac caatctcctc ctccaattct cctcctctcc ttccaaattc tagggttttg     240

cttgtatctc accccctttc tcaattccct agggaaactg tgaatttcat caaattccat     300

tattttttgg tcacaccctt aaagagatct gagagttcta aagatgatga cagatttatc     360
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tctcacgaga gatgaagatg aagaagaagc aaagccctta gcagaagaag aaggagcgcg      420

tgaagtagca gacagagagc acatgttcga caaagttgtg actccaagtg atgtcggaaa      480

actaaaccga cttgtgatcc caaagcaaca cgcagagaga ttcttccctt tagattcatc      540

ttcaaacgag aaaggtttgc ttttaaactt cgaagatctc actggcaaat cttggaggtt      600

ccgttactct tactggaaca gtagtcaaag ctatgtcatg actaaaggtt ggagcagatt      660

cgttaaagac aaaaagcttg acgccggaga tattgtctct ttccaaagat gtgtcggaga      720

ttcaggaaga gatagccgtt tgtttattga ttggaggaga agacctaaag tccctgacca      780

tcctcatttc gccgccggag ctatgttccc taggttttac agctttcctt cgaccaatta      840

cagtctttat aatcatcagc agcaacgtca tcatcacagt ggtggtggtt ataattatca      900

tcaaattccg agagaatttg gttatggtta cttcgttagg tcagtggatc agaggaacaa      960

tcctgcggct gcggtggctg atccgttggt gattgaatct gtgccggtga tgatgcacgg     1020

gagagctaat caggaacttg ttggaacggc cgggaagaga ctgaggcttt ttggagttga     1080

tatggaatgc ggcgagagcg gaatgaccaa cagtacggag gaggaatcat catcttccgg     1140

tggaagtttg ccacgtggag gcggtggtgg tgcttcatct tcctctttct ttcagctgag     1200

acttggaagc agcagtgaag atgatcactt cactaagaaa ggaaagtctt cattgtcttt     1260

tgatttggat caataataat gatgatgatg aaattagttg gtattttaag aaaaaaaaca     1320

tacatatata attctatata tatgacaaca taatgcattg atttcctt                  1368


<210>  14
<211>  310
<212>  PRT
<213>  Arabidopsis thaliana

<220>
<223> G1010 polypeptide

<400>  14

Met Met Thr Asp Leu Ser Leu Thr Arg Asp Glu Asp Glu Glu Glu Ala
1               5                   10                  15


Lys Pro Leu Ala Glu Glu Glu Gly Ala Arg Glu Val Ala Asp Arg Glu
            20                  25                  30


His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn
        35                  40                  45


Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Phe Phe Pro Leu Asp
    50                  55                  60


Ser Ser Ser Asn Glu Lys Gly Leu Leu Leu Asn Phe Glu Asp Leu Thr
```

```
65                  70                  75                  80


Gly Lys Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
                85                  90                  95


Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Asp Lys Lys Leu
            100                 105                 110


Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Cys Val Gly Asp Ser Gly
        115                 120                 125


Arg Asp Ser Arg Leu Phe Ile Asp Trp Arg Arg Arg Pro Lys Val Pro
    130                 135                 140


Asp His Pro His Phe Ala Ala Gly Ala Met Phe Pro Arg Phe Tyr Ser
145                 150                 155                 160


Phe Pro Ser Thr Asn Tyr Ser Leu Tyr Asn His Gln Gln Gln Arg His
                165                 170                 175


His His Ser Gly Gly Gly Tyr Asn Tyr His Gln Ile Pro Arg Glu Phe
            180                 185                 190


Gly Tyr Gly Tyr Phe Val Arg Ser Val Asp Gln Arg Asn Asn Pro Ala
        195                 200                 205


Ala Ala Val Ala Asp Pro Leu Val Ile Glu Ser Val Pro Val Met Met
    210                 215                 220


His Gly Arg Ala Asn Gln Glu Leu Val Gly Thr Ala Gly Lys Arg Leu
225                 230                 235                 240


Arg Leu Phe Gly Val Asp Met Glu Cys Gly Glu Ser Gly Met Thr Asn
                245                 250                 255


Ser Thr Glu Glu Glu Ser Ser Ser Ser Gly Gly Ser Leu Pro Arg Gly
            260                 265                 270


Gly Gly Gly Gly Ala Ser Ser Ser Ser Phe Phe Gln Leu Arg Leu Gly
        275                 280                 285


Ser Ser Ser Glu Asp Asp His Phe Thr Lys Lys Gly Lys Ser Ser Leu
    290                 295                 300


Ser Phe Asp Leu Asp Gln
305                 310
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<210> 15
<211> 1065
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2690

<400> 15
atggatatgg acgagatgag caatgtagcc aagacaacga cagagacttc aggcttaact   60

gactctgtct tgagcctcac gaaacgcatg aaacctactg aggttacgac caccacaaaa   120

cctgccttgt ccaacacgac gaaattcaaa ggagttgttc agcaacagaa cggtcattgg   180

ggtgctcaga tttacgcaga ccatcgaagg atttggcttg gaactttcaa atccgctcat   240

gaagccgctg ctgcttacga tagcgcatcg attaagcttc gaagctttga tgctaactcg   300

caccggaact tcccttggtc tgattttacc ctccatgaac cggactttca agagtgctac   360

acgacagaag ctgtgttgaa catgatcaga gacggttctt atcaacacaa gttcagagat   420

tttctcagaa tccggtctca gattgttgcg aatatcaaca tcgtgggatc aaaacaagtc   480

ttaggaggag gagaaggtgg tcaagaatcg aacaagtgtt tctcgtgcac gcagcttttt   540

cagaaagaac tgacaccgag cgatgtaggg aaactgaata ggcttgtgat acctaagaag   600

tatgcagtga agtatatgcc tttcataagc gatgatcaaa gcgagaaaga gacgagtgaa   660

ggagtagaag atgtggaggt tgtcttttac gacagagcaa tgagacaatg gaagtttagg   720

tattgttact ggagaagtag ccagagcttt gtcttcacca gaggatggaa tggtttcgtg   780

aaggagaaga atctcaagga gaaagatatt attgtctttt acacttgcga tgtccccaac   840

aatgtgaaga cattagaagg ccaaagcaag accttcttga tgattgatgt tcatcacttt   900

tcaggcaacg gtttcgtggt tcccgaggaa gtaaacaaga cggttcatga gatttctgat   960

gaagagatga aaacagaaac cctctttacc tcgaaggtag aagaagaaac caaatcagag   1020

gagaagaaag gagggtttat gctgtttggt gttaggatcc aatag   1065

<210> 16
<211> 354
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G2690 polypeptide

<400> 16

Met Asp Met Asp Glu Met Ser Asn Val Ala Lys Thr Thr Thr Glu Thr
1   5   10   15

Ser Gly Leu Thr Asp Ser Val Leu Ser Leu Thr Lys Arg Met Lys Pro
            20   25   30

```
Thr Glu Val Thr Thr Thr Thr Lys Pro Ala Leu Ser Asn Thr Thr Lys
        35                  40                  45


Phe Lys Gly Val Val Gln Gln Gln Asn Gly His Trp Gly Ala Gln Ile
    50                  55                  60


Tyr Ala Asp His Arg Arg Ile Trp Leu Gly Thr Phe Lys Ser Ala His
65                  70                  75                  80


Glu Ala Ala Ala Ala Tyr Asp Ser Ala Ser Ile Lys Leu Arg Ser Phe
                85                  90                  95


Asp Ala Asn Ser His Arg Asn Phe Pro Trp Ser Asp Phe Thr Leu His
            100                 105                 110


Glu Pro Asp Phe Gln Glu Cys Tyr Thr Thr Glu Ala Val Leu Asn Met
        115                 120                 125


Ile Arg Asp Gly Ser Tyr Gln His Lys Phe Arg Asp Phe Leu Arg Ile
    130                 135                 140


Arg Ser Gln Ile Val Ala Asn Ile Asn Ile Val Gly Ser Lys Gln Val
145                 150                 155                 160


Leu Gly Gly Gly Glu Gly Gly Gln Glu Ser Asn Lys Cys Phe Ser Cys
                165                 170                 175


Thr Gln Leu Phe Gln Lys Glu Leu Thr Pro Ser Asp Val Gly Lys Leu
            180                 185                 190


Asn Arg Leu Val Ile Pro Lys Lys Tyr Ala Val Lys Tyr Met Pro Phe
        195                 200                 205


Ile Ser Asp Asp Gln Ser Glu Lys Glu Thr Ser Glu Gly Val Glu Asp
    210                 215                 220


Val Glu Val Val Phe Tyr Asp Arg Ala Met Arg Gln Trp Lys Phe Arg
225                 230                 235                 240


Tyr Cys Tyr Trp Arg Ser Ser Gln Ser Phe Val Phe Thr Arg Gly Trp
                245                 250                 255


Asn Gly Phe Val Lys Glu Lys Asn Leu Lys Glu Lys Asp Ile Ile Val
            260                 265                 270


Phe Tyr Thr Cys Asp Val Pro Asn Asn Val Lys Thr Leu Glu Gly Gln
        275                 280                 285
```

```
Ser Lys Thr Phe Leu Met Ile Asp Val His His Phe Ser Gly Asn Gly
    290                 295                 300


Phe Val Val Pro Glu Glu Val Asn Lys Thr Val His Glu Ile Ser Asp
305                 310                 315                 320


Glu Glu Met Lys Thr Glu Thr Leu Phe Thr Ser Lys Val Glu Glu Glu
                325                 330                 335


Thr Lys Ser Glu Glu Lys Lys Gly Gly Phe Met Leu Phe Gly Val Arg
            340                 345                 350


Ile Gln



<210>  17
<211>  1253
<212>  DNA
<213>  Glycine max

<220>
<223> G3451 GLYMA-28NOV01-CLUSTER19062_3 Predicted polypeptide sequence is or
thologous to G867, G9, G993, G1930

<400>  17
ctagaatccg tacaatctaa tcaacataac aaaaatggat gcaattagtt gcatggatga      60

gagcaccacc actgagtcac tctctataag tctttctccg acgtcatcgt cggagaaagc     120

gaagccttct tcgatgatta catcgtcgga gaaggtttct ctgtccccgc cgccgtcaaa     180

cagactatgc cgtgttggaa gcggcgcgag cgcagtcgtg gatcctgatg gcggcggcag     240

cggcgctgag gtagagtcgc ggaaactccc ctcgtcgaag tacaagggcg tggtgcccca     300

gcccaacggc cgctggggtg cgcagattta cgagaagcac cagcgcgtgt ggcttggaac     360

gttcaacgag gaagacgagg cggcgcgtgc gtacgacatc gccgcgcagc ggttccgcgg     420

caaggacgcc gtcacgaact tcaagccgct cgccggcgcc gacgacgacg acggagaatc     480

ggagtttctc aactcgcatt ccaaacccga gatcgtcgac atgctgcgaa agcacacgta     540

caatgacgag ctggagcaga gcaagcgcag ccgcggcgtc gtccggcggc gaggctccgc     600

cgccgccggc accgcaaact caatttccgg cgcgtgcttt actaaggcac gtgagcagct     660

attcgagaag gctgttacgc cgagcgacgt tgggaaattg aaccgtttgg tgataccgaa     720

gcagcacgcg gagaagcact ttccgttaca gagctctaac ggcgttagcg cgacgacgat     780

agcggcggtg acggcgacgc cgacggcggc gaagggcgtt ttgttgaact tcgaagacgt     840

tggagggaaa gtgtggcggt ttcgttactc gtattggaac agtagccaga gttacgtctt     900

aaccaaaggt tggagccggt tcgttaagga gaagaatctg aaagctggtg acacggtttg     960
```

```
ttttcaccgg tccactggac cggacaagca gctttacatc gattggaaga cgaggaatgt   1020

tgttaacaac gaggtcgcgt tgttcggacc ggtcggaccg gttgtcgaac cgatccagat   1080

ggttcggctc tttggggtta acattttgaa actacccggt tcagatacta ttgttggcaa   1140

taacaataat gcaagtgggt gctgcaatgg caagagaaga gaaatggaac tgttctcgtt   1200

agagtgtagc aagaaaccta agattattgg tgctttgtaa cgttacgtta ggc          1253


<210>  18
<211>  401
<212>  PRT
<213>  Glycine max

<220>
<223> G3451 polypeptide GLYMA-28NOV01-CLUSTER19062_3  Orthologous to G867, G9
, G993, G1930

<400>  18

Met Asp Ala Ile Ser Cys Met Asp Glu Ser Thr Thr Thr Glu Ser Leu
1               5                   10                  15


Ser Ile Ser Leu Ser Pro Thr Ser Ser Ser Glu Lys Ala Lys Pro Ser
            20                  25                  30


Ser Met Ile Thr Ser Ser Glu Lys Val Ser Leu Ser Pro Pro Pro Ser
        35                  40                  45


Asn Arg Leu Cys Arg Val Gly Ser Gly Ala Ser Ala Val Val Asp Pro
    50                  55                  60


Asp Gly Gly Gly Ser Gly Ala Glu Val Glu Ser Arg Lys Leu Pro Ser
65                  70                  75                  80


Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala
                85                  90                  95


Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu
            100                 105                 110


Glu Asp Glu Ala Ala Arg Ala Tyr Asp Ile Ala Ala Gln Arg Phe Arg
        115                 120                 125


Gly Lys Asp Ala Val Thr Asn Phe Lys Pro Leu Ala Gly Ala Asp Asp
    130                 135                 140


Asp Asp Gly Glu Ser Glu Phe Leu Asn Ser His Ser Lys Pro Glu Ile
145                 150                 155                 160
```

```
Val Asp Met Leu Arg Lys His Thr Tyr Asn Asp Glu Leu Glu Gln Ser
                165                 170                 175

Lys Arg Ser Arg Gly Val Val Arg Arg Arg Gly Ser Ala Ala Ala Gly
            180                 185                 190

Thr Ala Asn Ser Ile Ser Gly Ala Cys Phe Thr Lys Ala Arg Glu Gln
        195                 200                 205

Leu Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg
    210                 215                 220

Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Gln Ser
225                 230                 235                 240

Ser Asn Gly Val Ser Ala Thr Thr Ile Ala Ala Val Thr Ala Thr Pro
                245                 250                 255

Thr Ala Ala Lys Gly Val Leu Leu Asn Phe Glu Asp Val Gly Gly Lys
            260                 265                 270

Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
        275                 280                 285

Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Lys Ala
    290                 295                 300

Gly Asp Thr Val Cys Phe His Arg Ser Thr Gly Pro Asp Lys Gln Leu
305                 310                 315                 320

Tyr Ile Asp Trp Lys Thr Arg Asn Val Val Asn Asn Glu Val Ala Leu
                325                 330                 335

Phe Gly Pro Val Gly Pro Val Val Glu Pro Ile Gln Met Val Arg Leu
            340                 345                 350

Phe Gly Val Asn Ile Leu Lys Leu Pro Gly Ser Asp Thr Ile Val Gly
        355                 360                 365

Asn Asn Asn Asn Ala Ser Gly Cys Cys Asn Gly Lys Arg Arg Glu Met
    370                 375                 380

Glu Leu Phe Ser Leu Glu Cys Ser Lys Lys Pro Lys Ile Ile Gly Ala
385                 390                 395                 400

Leu
```

<210> 19
<211> 1067
<212> DNA
<213> Oryza sativa

<220>
<223> ORYSA-22JAN02-CLUSTER46187_2 Predicted polypeptide sequence is orthologous to G867, G9, G993, G1930

<400> 19

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gcacgagcac ctgctttggc ttctccctct tcactgccct aattccttgc ttctctctcc      60

tctcctctct ctctctctct ctctctcgct gcagccatag cttagctttc ttggtgccaa     120

gatgggggtg gtcagcttct cctcgacttc ctccggcgcg tccactgcca ccaccgagtc     180

cggcggcgcc gtgcggatgt cgccggagcc ggtggtggcg gtggcggcgg cggctcaaca     240

gctgccggtg gtgaagggag ttgactcggc ggatgaggtg gtgacgtcga agcccgcagc     300

ggcggcggtg gcgcagcagt cgtcgaggta caagggggtg gtgccgcagc cgaacgggcg     360

gtgggggcg  cagatctacg agcgccacgc gcgggtgtgg ctcgggacgt tccccgacga     420

ggaggcggcg gcgcgggcct acgacgtggc ggcgctccgg taccgggggc gcgacgcggc     480

caccaacttc cccgggccg  cggcgtcggc ggccgagctc gcgttcctcg ccgcgcactc     540

caaggccgag atcgtcgaca tgctgcggaa gcacacctac gccgacgagc tccgccaggg     600

cctccgccgc ggccgcggca tgggcgcccg cgcccagccc acgccatcgt gggcgcgcga     660

gccgctgttc gagaaggccg tgacgcccag cgacgtcggc aagctcaacc gcctcgtggt     720

gcccaagcag cacgccgaga agcacttccc gctccgccgc gcggcgagct ccgactccgc     780

ctccgccgcc gccaccggca agggcgtgct cctcaacttc gaggacggcg agggcaaggt     840

gtggcgattc cggtactcgt actggaacag cagccagagc tacgtgctga ccaaggggtg     900

gagccgattc gtgagggaga agggcctccg cgccggcgac accattgtct tctccccgct     960

cggcgtacgg ccccgacaag ctgctcttca tcgactgcaa gaagaacaac gcggcggtgg    1020

cggcgaccac cacctgcgcc ggcgacgaga ggccaaccac aaccaca                  1067
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<210> 20
<211> 315
<212> PRT
<213> Oryza sativa

<220>
<223> ORYSA-22JAN02-CLUSTER46187_2 polypeptide Orthologous to G867, G9, G993, G1930

<400> 20

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Met Gly Val Val Ser Phe Ser Ser Thr Ser Ser Gly Ala Ser Thr Ala
1               5                   10                  15
```

```
Thr Thr Glu Ser Gly Gly Ala Val Arg Met Ser Pro Glu Pro Val Val
            20                  25                  30

Ala Val Ala Ala Ala Ala Gln Gln Leu Pro Val Val Lys Gly Val Asp
        35                  40                  45

Ser Ala Asp Glu Val Val Thr Ser Lys Pro Ala Ala Ala Ala Val Ala
    50                  55                  60

Gln Gln Ser Ser Arg Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg
65                  70                  75                  80

Trp Gly Ala Gln Ile Tyr Glu Arg His Ala Arg Val Trp Leu Gly Thr
                85                  90                  95

Phe Pro Asp Glu Glu Ala Ala Ala Arg Ala Tyr Asp Val Ala Ala Leu
            100                 105                 110

Arg Tyr Arg Gly Arg Asp Ala Ala Thr Asn Phe Pro Gly Ala Ala Ala
        115                 120                 125

Ser Ala Ala Glu Leu Ala Phe Leu Ala Ala His Ser Lys Ala Glu Ile
    130                 135                 140

Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Leu Arg Gln Gly
145                 150                 155                 160

Leu Arg Arg Gly Arg Gly Met Gly Ala Arg Ala Gln Pro Thr Pro Ser
                165                 170                 175

Trp Ala Arg Glu Pro Leu Phe Glu Lys Ala Val Thr Pro Ser Asp Val
            180                 185                 190

Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln His Ala Glu Lys His
        195                 200                 205

Phe Pro Leu Arg Arg Ala Ala Ser Ser Asp Ser Ala Ser Ala Ala Ala
    210                 215                 220

Thr Gly Lys Gly Val Leu Leu Asn Phe Glu Asp Gly Glu Gly Lys Val
225                 230                 235                 240

Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu
                245                 250                 255

Thr Lys Gly Trp Ser Arg Phe Val Arg Glu Lys Gly Leu Arg Ala Gly
            260                 265                 270
```

```
Asp Thr Ile Val Phe Ser Pro Leu Gly Val Arg Pro Arg Gln Ala Ala
        275                 280                 285


Leu His Arg Leu Gln Glu Glu Gln Arg Gly Gly Gly Gly Asp His His
    290                 295                 300


Leu Arg Arg Arg Arg Glu Ala Asn His Asn His
305                 310                 315


<210>  21
<211>  1081
<212>  DNA
<213>  Glycine max

<220>
<223> G3452 CLUSTER19062_7  Predicted polypeptide sequence is orthologous to
G867, G9, G993, G1930

<400>  21
caccaacaca aaatggatgg aggctgtgtc acagacgaaa ccaccacatc cagcgactct      60

ctttccgttc cgccgcccag ccgcgtcggc agcgttgcaa gcgccgtcgt cgaccccgac     120

ggttgttgcg tttccggcga ggccgaatcc cggaaactcc cttcgtcgaa atacaaaggc     180

gtggtgccgc aaccgaacgg tcgctgggga gctcagattt acgagaagca ccagcgcgtg     240

tggctcggca ctttcaacga ggaagacgaa gccgccagag cctacgacat cgccgcgctg     300

cgcttccgcg gccccgacgc cgtcaccaac ttcaagcctc ccgccgcctc cgacgacgcc     360

gagtccgagt tcctcaactc gcattccaag ttcgagatcg tcgacatgct ccgcaagcac     420

acctacgacg acgagctcca gcagagcacg cgcggtggta ggcgccgcct cgacgctgac     480

accgcgtcga gcggtgtgtt cgacgcgaaa gcgcgtgagc agctgttcga gaaaacggtt     540

acgccgagcg acgtcgggaa gctgaatcga ttagtgatac cgaagcagca cgcggagaag     600

cactttccgt taagcggatc cggcgacgaa agctcgccgt gcgtggcggg ggcttcggcg     660

gcgaagggaa tgttgttgaa ctttgaggac gttggaggga aagtgtggcg gtttcgttac     720

tcttattgga acagtagcca gagctacgtg cttaccaaag gatggagccg gttcgttaag     780

gagaagaatc ttcgagccgg tgacgcggtt cagttcttca agtcgaccgg accggaccgg     840

cagctatata tagactgcaa ggcgaggagt ggtgaggtta acaataatgc tggcggtttg     900

tttgttccga ttggaccggt cgttgagccg gttcagatgg ttcggctttt cggggtcaac     960

cttttgaaac tacccgtacc cggttcggat ggtgtaggga agagaaaaga gatggaactg    1020

tttgcatttg aatgttgcaa gaagttaaaa gtaattggag ctttgtaaca ttacatagtg    1080

c                                                                    1081


<210>  22
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<211>  351
<212>  PRT
<213>  Glycine max

<220>
<223> G3452 polypeptide CLUSTER19062_7  Orthologous to G867, G9, G993, G1930

<400>  22

Met Asp Gly Gly Cys Val Thr Asp Glu Thr Thr Thr Ser Ser Asp Ser
1               5                   10                  15


Leu Ser Val Pro Pro Pro Ser Arg Val Gly Ser Val Ala Ser Ala Val
            20                  25                  30


Val Asp Pro Asp Gly Cys Cys Val Ser Gly Glu Ala Glu Ser Arg Lys
        35                  40                  45


Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg
    50                  55                  60


Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr
65                  70                  75                  80


Phe Asn Glu Glu Asp Glu Ala Ala Arg Ala Tyr Asp Ile Ala Ala Leu
                85                  90                  95


Arg Phe Arg Gly Pro Asp Ala Val Thr Asn Phe Lys Pro Pro Ala Ala
            100                 105                 110


Ser Asp Asp Ala Glu Ser Glu Phe Leu Asn Ser His Ser Lys Phe Glu
        115                 120                 125


Ile Val Asp Met Leu Arg Lys His Thr Tyr Asp Asp Glu Leu Gln Gln
    130                 135                 140


Ser Thr Arg Gly Gly Arg Arg Arg Leu Asp Ala Asp Thr Ala Ser Ser
145                 150                 155                 160


Gly Val Phe Asp Ala Lys Ala Arg Glu Gln Leu Phe Glu Lys Thr Val
                165                 170                 175


Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
            180                 185                 190


His Ala Glu Lys His Phe Pro Leu Ser Gly Ser Gly Asp Glu Ser Ser
        195                 200                 205


Pro Cys Val Ala Gly Ala Ser Ala Ala Lys Gly Met Leu Leu Asn Phe
    210                 215                 220
```

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Glu Asp Val Gly Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
225                 230                 235                 240


Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys
                245                 250                 255


Glu Lys Asn Leu Arg Ala Gly Asp Ala Val Gln Phe Phe Lys Ser Thr
            260                 265                 270


Gly Pro Asp Arg Gln Leu Tyr Ile Asp Cys Lys Ala Arg Ser Gly Glu
        275                 280                 285


Val Asn Asn Asn Ala Gly Gly Leu Phe Val Pro Ile Gly Pro Val Val
    290                 295                 300


Glu Pro Val Gln Met Val Arg Leu Phe Gly Val Asn Leu Leu Lys Leu
305                 310                 315                 320


Pro Val Pro Gly Ser Asp Gly Val Gly Lys Arg Lys Glu Met Glu Leu
                325                 330                 335


Phe Ala Phe Glu Cys Cys Lys Lys Leu Lys Val Ile Gly Ala Leu
            340                 345                 350


<210>  23
<211>  1089
<212>  DNA
<213>  Glycine max

<220>
<223> G3453  Predicted polypeptide sequence is orthologous to G867, G9, G993,
 G1930

<400>  23
atggatggag gcagtgtcac agacgaaacc accacaacca gcaactctct ttcggttccg      60

gcgaatctat ctccgccgcc tctcagcctt gacggaagcg gcgcaaccgc cgtcgtctac     120

cccgacggtt gttgcgtctc cggcgaagcc gaatcccgga aactcccgtc ctcgaaatac     180

aaaggcgtgg tgccgcaacc gaacggtcgt tggggagctc agatttacga gaagcaccag     240

cgcgtgtggc tcggcacctt caacgaggaa gacgaagccg tcagagccta cgacatcgtc     300

gcgcatcgct tccgcggccg cgacgccgtc actaacttca agcctctcgc cggcgccgac     360

gacgccgaag ccgagttcct cagcacgcat tccaagtccg agatcgtcga catgctccgc     420

aggcacacct acgacaacga gctccagcag agcacccgcg gcggcaggcg ccgccgggac     480

gccgaaaccg cgtcgagcgg cgcgttcgac gcgaaggcgc gtgagcagct ggtcgagaaa     540

accgttacgc cgagcgacgt cgggaagctg aaccgattag tgataccaaa gcagcacgcg     600
```

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gagaagcact ttccgttaag cggatccggc ggcggagcct tgccgtgcat ggcggcggct     660

gcgggggcga aaggaatgtt gctgaacttt gaggacgttg gagggaaagt gtggcggttc     720

cgttactcgt attggaacag tagccagagc tacgtgctta ccaaaggatg gagccggttc     780

gttaaggaga agaatcttcg agctggtgac gcggttcagt tcttcaagtc gaccggactg     840

gaccggcaac tatatataga ctgcaaggcg aggagtggta aggttaacaa taatgctgcc     900

ggtttgttta ttccggttgg accggttgtt gagccggttc agatggtacg gcttttcggg     960

gtcgaccttt tgaaactacc cgtacccggt tcggatggta ttggggttgg ctgtgacggg    1020

aagagaaaag agatggagct gtttgcattt gaatgtagca agaagttaaa agtaattgga    1080

gctttgtaa                                                            1089


<210>  24
<211>  362
<212>  PRT
<213>  Glycine max

<220>
<223> G3453 polypeptide Orthologous to G867, G9, G993, G1930

<400>  24

Met Asp Gly Gly Ser Val Thr Asp Glu Thr Thr Thr Thr Ser Asn Ser
1               5                   10                  15


Leu Ser Val Pro Ala Asn Leu Ser Pro Pro Pro Leu Ser Leu Asp Gly
            20                  25                  30


Ser Gly Ala Thr Ala Val Val Tyr Pro Asp Gly Cys Cys Val Ser Gly
        35                  40                  45


Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val
    50                  55                  60


Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln
65                  70                  75                  80


Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Val Arg Ala
                85                  90                  95


Tyr Asp Ile Val Ala His Arg Phe Arg Gly Arg Asp Ala Val Thr Asn
            100                 105                 110


Phe Lys Pro Leu Ala Gly Ala Asp Asp Ala Glu Ala Glu Phe Leu Ser
        115                 120                 125


Thr His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Arg His Thr Tyr
```

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    130                 135                 140


Asp Asn Glu Leu Gln Gln Ser Thr Arg Gly Gly Arg Arg Arg Arg Asp
145                 150                 155                 160


Ala Glu Thr Ala Ser Ser Gly Ala Phe Asp Ala Lys Ala Arg Glu Gln
                165                 170                 175


Leu Val Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg
            180                 185                 190


Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Ser Gly
        195                 200                 205


Ser Gly Gly Gly Ala Leu Pro Cys Met Ala Ala Ala Ala Gly Ala Lys
    210                 215                 220


Gly Met Leu Leu Asn Phe Glu Asp Val Gly Gly Lys Val Trp Arg Phe
225                 230                 235                 240


Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
                245                 250                 255


Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Ala Val
            260                 265                 270


Gln Phe Phe Lys Ser Thr Gly Leu Asp Arg Gln Leu Tyr Ile Asp Cys
        275                 280                 285


Lys Ala Arg Ser Gly Lys Val Asn Asn Asn Ala Ala Gly Leu Phe Ile
    290                 295                 300


Pro Val Gly Pro Val Val Glu Pro Val Gln Met Val Arg Leu Phe Gly
305                 310                 315                 320


Val Asp Leu Leu Lys Leu Pro Val Pro Gly Ser Asp Gly Ile Gly Val
                325                 330                 335


Gly Cys Asp Gly Lys Arg Lys Glu Met Glu Leu Phe Ala Phe Glu Cys
            340                 345                 350


Ser Lys Lys Leu Lys Val Ile Gly Ala Leu
        355                 360


<210>  25
<211>  1188
<212>  DNA
<213>  Glycine max
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<220>
<223> G3454 Predicted polypeptide sequence is orthologous to G867, G9, G993, G1930

<400> 25
atggatgcaa ttagttgcat ggatgagagc accaccaccg agtcactctc cataagtcag 60

gcgaagcctt cttcgacgat tatgtcgtcc gagaaggctt ctccttcccc gccgccgccg 120

aacaggctgt gccgcgtcgg tagcggtgct agcgcagtcg tggattccga cggcggcggc 180

gggggtggca gcaccgaggt ggagtcgcgg aagctcccct cgtccaagta taagggcgtc 240

gtgccccagc ccaacggccg ctggggctcg cagatttacg agaagcacca gcgcgtgtgg 300

ctgggaacgt tcaacgagga agacgaggcg gcgcgtgcgt acgacgtcgc cgtgcagcga 360

ttccgcggca aggactccgt cacgaacttc aagccgctcg ccggcgccga cgacgacgac 420

ggagaatcgg agtttctcaa ctcgcattcc aaacccgaga tcgtcgacat gctgcgaaag 480

cacacgtaca atgacgagct ggagcatagc aagcgcaacc gcggcgtcgt ccggcggcga 540

ggctccgccg ccgtcggcac cgcagactca atttccggcg cgtgctttac taatgcacgt 600

gagcagctat tcgagaaagc tgttacgccg agcgacgttt ggaaattgaa ccgtttggtg 660

ataccgaagc agcacgcgga gaagcacttt ccgttacaga gctctaacgg cgttagcgcg 720

acgacgatag cggcggtgac ggcgacgccg acggcggcga agggcgtttt gttgaacttc 780

gaagacgttg gagggaaagt gtggcggttt cgttactcgt attggaacag tagccagagt 840

tacgtcttaa ccaaaggttg gagccggttc gttaaggaga agaatctgaa agctggtgac 900

acggtttgtt ttcaccggtc cactggaccg gacaagcagc tttacatcga ttggaagacg 960

aggaatgttg ttaacaacga ggtcgcgttg ttcggaccgg tcggaccggt tgtcgaaccg 1020

atccagatgg ttcggctctt tggggttaac attttgaaac tacccggttc agatactatt 1080

gttggcaata acaataatgc aagtgggtgc tgcaatggca agagaagaga aatggaactg 1140

ttctcgttag agtgtagcaa gaaacctaag attattggtg ctttgtaa 1188

<210> 26
<211> 395
<212> PRT
<213> Glycine max

<220>
<223> G3454 polypeptide Orthologous to G867, G9, G993, G1930

<400> 26

Met Asp Ala Ile Ser Cys Met Asp Glu Ser Thr Thr Thr Glu Ser Leu
1   5   10   15

Ser Ile Ser Gln Ala Lys Pro Ser Ser Thr Ile Met Ser Ser Glu Lys
            20   25   30

```
Ala Ser Pro Ser Pro Pro Pro Pro Asn Arg Leu Cys Arg Val Gly Ser
        35                  40                  45

Gly Ala Ser Ala Val Val Asp Ser Asp Gly Gly Gly Gly Gly Gly Ser
    50                  55                  60

Thr Glu Val Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val
65                  70                  75                  80

Val Pro Gln Pro Asn Gly Arg Trp Gly Ser Gln Ile Tyr Glu Lys His
                85                  90                  95

Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala Arg
            100                 105                 110

Ala Tyr Asp Val Ala Val Gln Arg Phe Arg Gly Lys Asp Ser Val Thr
        115                 120                 125

Asn Phe Lys Pro Leu Ala Gly Ala Asp Asp Asp Asp Gly Glu Ser Glu
    130                 135                 140

Phe Leu Asn Ser His Ser Lys Pro Glu Ile Val Asp Met Leu Arg Lys
145                 150                 155                 160

His Thr Tyr Asn Asp Glu Leu Glu His Ser Lys Arg Asn Arg Gly Val
                165                 170                 175

Val Arg Arg Arg Gly Ser Ala Ala Val Gly Thr Ala Asp Ser Ile Ser
            180                 185                 190

Gly Ala Cys Phe Thr Asn Ala Arg Glu Gln Leu Phe Glu Lys Ala Val
        195                 200                 205

Thr Pro Ser Asp Val Trp Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
    210                 215                 220

His Ala Glu Lys His Phe Pro Leu Gln Ser Ser Asn Gly Val Ser Ala
225                 230                 235                 240

Thr Thr Ile Ala Ala Val Thr Ala Thr Pro Thr Ala Ala Lys Gly Val
                245                 250                 255

Leu Leu Asn Phe Glu Asp Val Gly Gly Lys Val Trp Arg Phe Arg Tyr
            260                 265                 270

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
```

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        275                 280                 285


Arg Phe Val Lys Glu Lys Asn Leu Lys Ala Gly Asp Thr Val Cys Phe
    290                 295                 300


His Arg Ser Thr Gly Pro Asp Lys Gln Leu Tyr Ile Asp Trp Lys Thr
305                 310                 315                 320


Arg Asn Val Val Asn Asn Glu Val Ala Leu Phe Gly Pro Val Gly Pro
                325                 330                 335


Val Val Glu Pro Ile Gln Met Val Arg Leu Phe Gly Val Asn Ile Leu
            340                 345                 350


Lys Leu Pro Gly Ser Asp Thr Ile Val Gly Asn Asn Asn Asn Ala Ser
        355                 360                 365


Gly Cys Cys Asn Gly Lys Arg Arg Glu Met Glu Leu Phe Ser Leu Glu
    370                 375                 380


Cys Ser Lys Lys Pro Lys Ile Ile Gly Ala Leu
385                 390                 395


<210>  27
<211>  1160
<212>  DNA
<213>  Glycine max

<220>
<223> G3455  GLYMA-28NOV01-CLUSTER19062_5   Predicted polypeptide sequence is
 orthologous to G867, G9, G993, G1930

<400>  27
atggatgcaa ttagttgcct ggatgagagc accaccaccg agtcactctc cataagtcag      60

gcgaagcctt cttcgacgat tatgtcgtcc gagaaggctt ctccttcccc gccgccgccg     120

aacaggctgt gccgcgtcgg tagcggtgct agcgcagtcg tggattccga cggcggcggc     180

gggggtggca gcaccgaggt ggagtcgcgg aagctcccct cgtccaagta taagggcgtc     240

gtgccccagc ccaacggccg ctggggctcg cagatttacg agaagcacca gcgcgtgtgg     300

ctgggaacgt tcaacgagga agacgaggcg gcgcgtgcgt acgacgtcgc cgtgcagcga     360

ttccgcggca aggacgccgt cacaaacttc aagccgctct ccggcaccga cgacgacgac     420

ggggaatcgg agtttctcaa ctcgcattcg aaatccgaga tcgtcgacat gctgcgtaag     480

catacgtaca atgacgagct ggaacaaagc aagcgcagcc gcggctttcg tacgttcgcc     540

gcggctccgc cggccggcgc cggaaacgga aactcaatct ccggcgcgtg tgttatgaag     600

gcgcgtgagc agctattcca gaaggccgtt acgccgagcg acgttgggaa actgaaccgt     660
```

```
ttggtgatac cgaagcagca cgcggagaag cactttcctt tacagagcgc tgctaacggc     720

gtttagcgcg acggcgaacg gcggcgaagg gcgttttgtt gaacttcgaa gacgttggag     780

ggaaagtgtg gcggtttcgt tactcgtatt ggaacagtag ccagagttac gtcttgacca     840

aaggttggag ccggttcgtt aaggagaaga atctgaaagc cggtgacacg gtttgttttc     900

aacggtccac tggaccggac aggcagcttt acatcgattg gaagacgagg aatgttgtta     960

acgaggtcgc gttgttcgga ccggttgtcg aaccgatcca gatggttcgg ctctttggtg    1020

ttaacatttt gaaactaccc ggttcagatt ctatcgccaa taacaataat gcaagtgggt    1080

gctgcaatgg caagagaaga gaaatggaac tcttttcatt agagtgtagc aagaaaccta    1140

agattattgg tgctttgtag                                                1160


<210>  28
<211>  241
<212>  PRT
<213>  Glycine max

<220>
<223> G3455 polypeptide GLYMA-28NOV01-CLUSTER19062_5   Orthologous to G867, G
9, G993, G1930

<400>  28

Met Asp Ala Ile Ser Cys Leu Asp Glu Ser Thr Thr Thr Glu Ser Leu
1               5                   10                  15


Ser Ile Ser Gln Ala Lys Pro Ser Ser Thr Ile Met Ser Ser Glu Lys
            20                  25                  30


Ala Ser Pro Ser Pro Pro Pro Pro Asn Arg Leu Cys Arg Val Gly Ser
        35                  40                  45


Gly Ala Ser Ala Val Val Asp Ser Asp Gly Gly Gly Gly Gly Gly Ser
    50                  55                  60


Thr Glu Val Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val
65                  70                  75                  80


Val Pro Gln Pro Asn Gly Arg Trp Gly Ser Gln Ile Tyr Glu Lys His
                85                  90                  95


Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala Arg
            100                 105                 110


Ala Tyr Asp Val Ala Val Gln Arg Phe Arg Gly Lys Asp Ala Val Thr
        115                 120                 125


Asn Phe Lys Pro Leu Ser Gly Thr Asp Asp Asp Asp Gly Glu Ser Glu
```

```
    130                 135                 140


Phe Leu Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys
145                 150                 155                 160


His Thr Tyr Asn Asp Glu Leu Glu Gln Ser Lys Arg Ser Arg Gly Phe
                165                 170                 175


Arg Thr Phe Ala Ala Ala Pro Pro Ala Gly Ala Gly Asn Gly Asn Ser
            180                 185                 190


Ile Ser Gly Ala Cys Val Met Lys Ala Arg Glu Gln Leu Phe Gln Lys
        195                 200                 205


Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
    210                 215                 220


Lys Gln His Ala Glu Lys His Phe Pro Leu Gln Ser Ala Ala Asn Gly
225                 230                 235                 240


Val



<210>  29
<211>  1291
<212>  DNA
<213>  Oryza sativa

<220>
<223> G3388 AP002913b  GI:12328560  Predicted polypeptide sequence is ortholo
gous to G867, G9, G993, G1930

<400>  29
ctagacactg ccctaattac aacccatttg cttatctctc tcctctctct ctctctctcg      60

ctgcagccat agcttagcta gagctagagc tttcttggtg ccgagatggg ggtggtcagc     120

ttctcctcga cttcctccgg cgcgtccacg gccaccaccg agtccggcgg cgccgtgcgg     180

atgtcgccgg agccggtggt ggcggtggcg gcggcggctc aacagctacc ggtggtgaag     240

ggagttgact cggcggatga ggtggtgacg tcgaggccgg cggcggcggc ggcgcagcag     300

tcgtcgcggt acaagggggt ggtgccgcag ccgaacggga ggtgggggc gcagatctac     360

gagcggcacg cgcgggtgtg gctcgggacg ttccccgacg aggaggcggc ggcgcgggcc     420

tacgacgtgg cggcgctccg gtaccggggg cgcgacgcgg ccaccaactt ccccggggcc     480

gcggcgtcgg ccgccgagct cgcgttcctc gccgcgcact ccaaggccga gatcgtcgac     540

atgctccgga agcacaccta cgccgacgag ctccgccagg ggctccgccg cggccgcggc     600

atgggcgccc gcgcccagcc cacgccgtcg tgggcgcgcg agccgctgtt cgagaaggcc     660
```

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gtgacgccca gcgacgtcgg caagctcaac cgcctcgtgg tgcccaagca gcacgccgag     720

aagcacttcc cgctccgccg cgcggcgagc tccgactccg cctccgccgc cgccaccggc     780

aagggcgtgc tcctcaactt cgaggacggc gaggggaagg tgtggcgatt ccggtactcg     840

tactggaaca gcagccagag ctacgtgctg accaaggggt ggagccgatt cgtgagggag     900

aagggcctcc gcgccggcga caccatagtc ttctcccgct cggcgtacgg ccccgacaag     960

ctgctcttca tcgactgcaa gaagaacaac gcggcggcgg cgaccaccac ctgcgccggc    1020

gacgagaggc caaccacaag cggcgccgaa ccacgcgtcg tgaggctctt cggcgtcgac    1080

atcgccggcg gcgattgccg gaagcgggag agggcggtgg agatggggca agaggtcttc    1140

ctactgaaga ggcaatgcgt ggttcatcag cgtactcctg ccctaggtgc cctgctgtta    1200

tagcatcaaa tcaaattcat atatagatca aatcaaatct tcttctcttc catctttttt    1260

gttgttcatc gtctgttgtt tcatcttcga g                                   1291


<210>  30
<211>  365
<212>  PRT
<213>  Oryza sativa

<220>
<223> G3388 polypeptide OSC21673.C1.p5.fg GI:12328560  Orthologous to G867, G
9, G993, G1930

<400>  30

Met Gly Val Val Ser Phe Ser Ser Thr Ser Ser Gly Ala Ser Thr Ala
1               5                   10                  15


Thr Thr Glu Ser Gly Gly Ala Val Arg Met Ser Pro Glu Pro Val Val
            20                  25                  30


Ala Val Ala Ala Ala Ala Gln Gln Leu Pro Val Val Lys Gly Val Asp
        35                  40                  45


Ser Ala Asp Glu Val Val Thr Ser Arg Pro Ala Ala Ala Ala Ala Gln
    50                  55                  60


Gln Ser Ser Arg Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp
65                  70                  75                  80


Gly Ala Gln Ile Tyr Glu Arg His Ala Arg Val Trp Leu Gly Thr Phe
                85                  90                  95


Pro Asp Glu Glu Ala Ala Ala Arg Ala Tyr Asp Val Ala Ala Leu Arg
            100                 105                 110


Tyr Arg Gly Arg Asp Ala Ala Thr Asn Phe Pro Gly Ala Ala Ala Ser
```

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        115                 120                 125

Ala Ala Glu Leu Ala Phe Leu Ala Ala His Ser Lys Ala Glu Ile Val
    130                 135                 140

Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Leu Arg Gln Gly Leu
145                 150                 155                 160

Arg Arg Gly Arg Gly Met Gly Ala Arg Ala Gln Pro Thr Pro Ser Trp
                165                 170                 175

Ala Arg Glu Pro Leu Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly
            180                 185                 190

Lys Leu Asn Arg Leu Val Val Pro Lys Gln His Ala Glu Lys His Phe
        195                 200                 205

Pro Leu Arg Arg Ala Ala Ser Ser Asp Ser Ala Ser Ala Ala Ala Thr
    210                 215                 220

Gly Lys Gly Val Leu Leu Asn Phe Glu Asp Gly Glu Gly Lys Val Trp
225                 230                 235                 240

Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr
                245                 250                 255

Lys Gly Trp Ser Arg Phe Val Arg Glu Lys Gly Leu Arg Ala Gly Asp
            260                 265                 270

Thr Ile Val Phe Ser Arg Ser Ala Tyr Gly Pro Asp Lys Leu Leu Phe
        275                 280                 285

Ile Asp Cys Lys Lys Asn Asn Ala Ala Ala Ala Thr Thr Thr Cys Ala
    290                 295                 300

Gly Asp Glu Arg Pro Thr Thr Ser Gly Ala Glu Pro Arg Val Val Arg
305                 310                 315                 320

Leu Phe Gly Val Asp Ile Ala Gly Gly Asp Cys Arg Lys Arg Glu Arg
                325                 330                 335

Ala Val Glu Met Gly Gln Glu Val Phe Leu Leu Lys Arg Gln Cys Val
            340                 345                 350

Val His Gln Arg Thr Pro Ala Leu Gly Ala Leu Leu Leu
        355                 360                 365
```

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<210>  31
<211>  1068
<212>  DNA
<213>  Oryza sativa

<220>
<223> G3389  AP002913  OSC21674.C1.p12.fg  Predicted polypeptide sequence is
orthologous to G867, G9, G993, G1930

<400>  31
gctaggctgt tctctctttc cattcgtcaa gaactaccac gacgtcgaca tcataatcgt      60

cagagagctc gagaaatttt ttagtatctt tgatccagat cgatcatgga gcaagaagct     120

gccatggtcg tcttctcctg caactccggc tccggtgggt cgtcgtcgac gaccgattca     180

aagcaagagg aggaggagga ggaggagttg gccgcaatgg aggaagacga gttgatccac     240

gtcgtccagg cggcggagct gcggctgccg tcgtcgacga cggcgacgcg gccgtcgtcg     300

cggtacaagg gggtggtgcc gcagccgaac gggcggtggg gggcgcagat ctacgagcgg     360

cacgcgcggg tgtggctcgg gacgttcccc gacgaggagg cggcggcgcg cgcctacgac     420

gtggcggcgc tccgcttccg gggcgcgac gccgtcacca accgcgcccc ggcggcggag     480

ggcgcgtccg ccggcgagct cgcgttcctg gccgcgcact ccaaggcgga ggtcgtggac     540

atgctgcgga agcacaccta cgacgacgag ctccagcagg gcctccgccg cggctcgcgc     600

gcgcagccga cgccgcggtg ggcgcgcgag ccgctgttcg agaaggccgt gacgccgagc     660

gacgtcggca agctcaaccg cctcgtggtg cccaagcagc aggccgagag gcatttcccg     720

ttcccgctcc gccgccacag ctccgacgcc gccggcaagg gcgtgctcct caacttcgag     780

gacggcgacg gcaaggtgtg gcgattccgg tactcgtact ggaacagcag ccagagttac     840

gtgctcacca aggggtggag ccgattcgtg agggagaagg gcctccgacc aggcgacacc     900

gtggccttct cccggtcggc ggcggcgtgg gggacggaga agcacctcct catcgactgc     960

aagaagatgg agaggaacaa cctggcaacc gtcgacgacg atgcccgtgt cgtcgtcaag    1020

ctgttcggcg ttgacatcgc cggagacaag acgaggtaac acgcaagc                 1068


<210>  32
<211>  317
<212>  PRT
<213>  Oryza sativa

<220>
<223> G3389 polypeptide BAB21211.1 OSC21674.C1.p12.fg Orthologous to G867, G9
, G993, G1930

<400>  32

Met Glu Gln Glu Ala Ala Met Val Val Phe Ser Cys Asn Ser Gly Ser
1               5                   10                  15


Gly Gly Ser Ser Ser Thr Thr Asp Ser Lys Gln Glu Glu Glu Glu Glu
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            20                  25                  30


Glu Glu Leu Ala Ala Met Glu Glu Asp Glu Leu Ile His Val Val Gln
        35                  40                  45


Ala Ala Glu Leu Arg Leu Pro Ser Ser Thr Thr Ala Thr Arg Pro Ser
    50                  55                  60


Ser Arg Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala
65                  70                  75                  80


Gln Ile Tyr Glu Arg His Ala Arg Val Trp Leu Gly Thr Phe Pro Asp
                85                  90                  95


Glu Glu Ala Ala Ala Arg Ala Tyr Asp Val Ala Ala Leu Arg Phe Arg
            100                 105                 110


Gly Arg Asp Ala Val Thr Asn Arg Ala Pro Ala Ala Glu Gly Ala Ser
        115                 120                 125


Ala Gly Glu Leu Ala Phe Leu Ala Ala His Ser Lys Ala Glu Val Val
    130                 135                 140


Asp Met Leu Arg Lys His Thr Tyr Asp Asp Glu Leu Gln Gln Gly Leu
145                 150                 155                 160


Arg Arg Gly Ser Arg Ala Gln Pro Thr Pro Arg Trp Ala Arg Glu Pro
                165                 170                 175


Leu Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg
            180                 185                 190


Leu Val Val Pro Lys Gln Gln Ala Glu Arg His Phe Pro Phe Pro Leu
        195                 200                 205


Arg Arg His Ser Ser Asp Ala Ala Gly Lys Gly Val Leu Leu Asn Phe
    210                 215                 220


Glu Asp Gly Asp Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
225                 230                 235                 240


Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Arg
                245                 250                 255


Glu Lys Gly Leu Arg Pro Gly Asp Thr Val Ala Phe Ser Arg Ser Ala
            260                 265                 270
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Ala Ala Trp Gly Thr Glu Lys His Leu Leu Ile Asp Cys Lys Lys Met
        275                 280                 285


Glu Arg Asn Asn Leu Ala Thr Val Asp Asp Asp Ala Arg Val Val Val
    290                 295                 300


Lys Leu Phe Gly Val Asp Ile Ala Gly Asp Lys Thr Arg
305                 310                 315


<210>  33
<211>  1348
<212>  DNA
<213>  Oryza sativa

<220>
<223> G3390 AC130725 Predicted polypeptide sequence is orthologous to G867, G
9, G993, G1930

<400>  33
cttcagaggc ttcacctttc atcagcttag ctagctagct gctcgatccg gcggcgtgat      60

cgatcgatct ctctgattct atcaggtgtt cgaccagatt ccatcgatgg acagcacgag     120

ctgtctcttg gacgacgcga gcagcggcgc gtccacgggc aagaaggcgg cggcggcggc     180

ggcgtcgaag gcgctgcagc gcgtgggcag cggcgccagc gcggtgatgg acgcggccga     240

gcctggcgcc gaggcggact cgggcggcga gcggcgcggc ggcggcggcg ggaagctgcc     300

gtcgtccaag tacaagggcg tggtgccgca accgaacggg cggtggggcg cgcagatata     360

cgagcggcac cagcgggtgt ggctcggcac gttcaccggc gaggcggagg cggcgcgcgc     420

ctacgacgtg gcggcgcagc ggttccgcgg ccgcgacgcc gtcaccaact tccgcccgct     480

cgccgagtcc gacccggagg ccgccgtcga gctccgcttc ctcgcgtccc gctccaaggc     540

cgaggtcgtc gacatgctcc gcaagcacac ctacctcgag gagctcacgc agaacaagcg     600

cgccttcgcc gccatctccc cgccgccccc caagcacccc gcctcctctc cgacgtcctc     660

ctccgccgcg cgcgagcacc tgttcgacaa gacggtgacg cccagcgacg tcgggaagct     720

gaaccggctg gtgatcccca agcagcacgc cgagaagcac ttcccgctcc agctccctcc     780

ccctaccaca acctcctccg tcgccgccgc cgccgacgcc gccgccggcg gcggcgattg     840

caagggcgtc ctcctcaact tcgaggacgc cgccgggaag gtgtggaaat tccggtactc     900

ctactggaac agcagccaga gctacgtgct caccaagggg tggagccgct tcgtcaagga     960

gaaggggctc cacgccggcg acgccgtcgg cttctaccgc gccgccggta agaacgcgca    1020

gctcttcatc gactgcaagg tccgggcaaa acccaccacc gccgccgccg ccgccgcctt    1080

cctcagcgcg gtggccgccg ccgccgcgcc gccacccgcc gtgaaggcta tcaggctgtt    1140

cggtgtcgac ctgctcacgg cggcggcgcc ggagctgcag gacgccggcg gcgccgccat    1200

gaccaagagc aagagagcca tggacgccat ggctgagtca caagcacacg tggtttttaa    1260
```

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gaagcaatgc atagagcttg cgctaaccta gctagcacgc tgatgcagct agcgtttttt   1320

ttgctcattc gcttgcttgc ttaattat                                      1348


<210>  34
<211>  394
<212>  PRT
<213>  Oryza sativa

<220>
<223> G3390 polypeptide Orthologous to G867, G9, G993, G1930

<400>  34

Met Asp Ser Thr Ser Cys Leu Leu Asp Asp Ala Ser Ser Gly Ala Ser
1               5                   10                  15


Thr Gly Lys Lys Ala Ala Ala Ala Ala Ala Ser Lys Ala Leu Gln Arg
            20                  25                  30


Val Gly Ser Gly Ala Ser Ala Val Met Asp Ala Ala Glu Pro Gly Ala
        35                  40                  45


Glu Ala Asp Ser Gly Gly Glu Arg Arg Gly Gly Gly Gly Gly Lys Leu
    50                  55                  60


Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp
65                  70                  75                  80


Gly Ala Gln Ile Tyr Glu Arg His Gln Arg Val Trp Leu Gly Thr Phe
                85                  90                  95


Thr Gly Glu Ala Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala Gln Arg
            100                 105                 110


Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Arg Pro Leu Ala Glu Ser
        115                 120                 125


Asp Pro Glu Ala Ala Val Glu Leu Arg Phe Leu Ala Ser Arg Ser Lys
    130                 135                 140


Ala Glu Val Val Asp Met Leu Arg Lys His Thr Tyr Leu Glu Glu Leu
145                 150                 155                 160


Thr Gln Asn Lys Arg Ala Phe Ala Ala Ile Ser Pro Pro Pro Pro Lys
                165                 170                 175


His Pro Ala Ser Ser Pro Thr Ser Ser Ser Ala Ala Arg Glu His Leu
            180                 185                 190
```

```
Phe Asp Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
        195                 200                 205

Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Gln Leu Pro
    210                 215                 220

Pro Pro Thr Thr Thr Ser Ser Val Ala Ala Ala Ala Asp Ala Ala Ala
225                 230                 235                 240

Gly Gly Gly Asp Cys Lys Gly Val Leu Leu Asn Phe Glu Asp Ala Ala
                245                 250                 255

Gly Lys Val Trp Lys Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
            260                 265                 270

Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Gly Leu
        275                 280                 285

His Ala Gly Asp Ala Val Gly Phe Tyr Arg Ala Ala Gly Lys Asn Ala
    290                 295                 300

Gln Leu Phe Ile Asp Cys Lys Val Arg Ala Lys Pro Thr Thr Ala Ala
305                 310                 315                 320

Ala Ala Ala Ala Phe Leu Ser Ala Val Ala Ala Ala Ala Ala Pro Pro
                325                 330                 335

Pro Ala Val Lys Ala Ile Arg Leu Phe Gly Val Asp Leu Leu Thr Ala
            340                 345                 350

Ala Ala Pro Glu Leu Gln Asp Ala Gly Gly Ala Ala Met Thr Lys Ser
        355                 360                 365

Lys Arg Ala Met Asp Ala Met Ala Glu Ser Gln Ala His Val Val Phe
    370                 375                 380

Lys Lys Gln Cys Ile Glu Leu Ala Leu Thr
385                 390


<210>  35
<211>  1338
<212>  DNA
<213>  Oryza sativa

<220>
<223> G3391 AP003450   OSC26104.C1.p13.fg  Predicted polypeptide sequence is
orthologous to G867, G9, G993, G1930

<400>  35
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ggagagtagg agtgtgctag tgtgtgaggt ctactgaaat ggacagctcc agctgcctgg 60

tggatgatac caacagcggc ggctcgtcca cggacaagct gagggcgttg gccgccgcgg 120

cggcggagac ggcgccgctg gagcgcatgg ggagcggggc gagcgcggtg gtggacgcgg 180

ccgagcctgg cgcggaggcg gactccgggt ccgggggacg tgtgtgcggc ggcggcggcg 240

gcggtgccgg cggtgcggga gggaagctgc cgtcgtccaa gttcaagggc gtcgtgccgc 300

agcccaacgg gaggtggggc gcgcagatct acgagcggca ccagcgggtg tggctcggca 360

cgttcgccgg ggaggacgac gccgcgcgcg cctacgacgt cgccgcgcag cgcttccgcg 420

gccgcgacgc cgtcaccaac ttccgcccgc tcgccgaggc cgacccggac gccgccgccg 480

agcttcgctt cctcgccacg cgctccaagg ccgaggtcgt cgacatgctc cgcaagcaca 540

cctacttcga cgagctcgcg cagagcaagc gcaccttcgc cgcctccacg ccgtcggccg 600

cgaccaccac cgcctccctc tccaacggcc acctctcgtc gccccgctcc cccttcgcgc 660

ccgccgcggc gcgcgaccac ctgttcgaca agacggtcac cccgagcgac gtgggcaagc 720

tgaacaggct cgtcataccg aagcagcacg ccgagaagca cttcccgcta cagctcccgt 780

ccgccggcgg cgagagcaag ggtgtcctcc tcaacttcga ggacgccgcc ggcaaggtgt 840

ggcggttccg gtactcgtac tggaacagca gccagagcta cgtgctaacc aagggctgga 900

gccgcttcgt caaggagaag ggtctccacg ccgacggcaa gctcttcatc gactgcaagt 960

tagtacggtc gaccggcgcc gccctcgcgt cgcccgctga tcagccagcg ccgtcgccgg 1020

tgaaggccgt caggctcttc ggcgtggacc tgctcacggc gccggcgccg gtcgaacaga 1080

tggccgggtg caagagagcc agggacttgg cggcgacgac gcctccacaa gcggcggcgt 1140

tcaagaagca atgcatagag ctggcactag tatagagtta gcactattag ctcgatcttc 1200

tctagctagt gtcttttttg ctcccatgca tcataattca ggtggtagct agcttagtcc 1260

cttgttgatc ctatctacta atctcacttg gttttttttg ttaatttatt cgcccatgtt 1320

cttgcttgct ttgctgta 1338

<210> 36
<211> 378
<212> PRT
<213> Oryza sativa

<220>
<223> G3391 polypeptide AP003450 OSC26104.C1.p13.fg Orthologous to G867, G9, G993, G1930

<400> 36

Met Asp Ser Ser Ser Cys Leu Val Asp Asp Thr Asn Ser Gly Gly Ser
1 5 10 15

Ser Thr Asp Lys Leu Arg Ala Leu Ala Ala Ala Ala Ala Glu Thr Ala

```
            20                  25                  30

Pro Leu Glu Arg Met Gly Ser Gly Ala Ser Ala Val Val Asp Ala Ala
        35                  40                  45

Glu Pro Gly Ala Glu Ala Asp Ser Gly Ser Gly Gly Arg Val Cys Gly
    50                  55                  60

Gly Gly Gly Gly Gly Ala Gly Gly Ala Gly Gly Lys Leu Pro Ser Ser
65                  70                  75                  80

Lys Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln
                85                  90                  95

Ile Tyr Glu Arg His Gln Arg Val Trp Leu Gly Thr Phe Ala Gly Glu
            100                 105                 110

Asp Asp Ala Ala Arg Ala Tyr Asp Val Ala Ala Gln Arg Phe Arg Gly
        115                 120                 125

Arg Asp Ala Val Thr Asn Phe Arg Pro Leu Ala Glu Ala Asp Pro Asp
    130                 135                 140

Ala Ala Ala Glu Leu Arg Phe Leu Ala Thr Arg Ser Lys Ala Glu Val
145                 150                 155                 160

Val Asp Met Leu Arg Lys His Thr Tyr Phe Asp Glu Leu Ala Gln Ser
                165                 170                 175

Lys Arg Thr Phe Ala Ala Ser Thr Pro Ser Ala Ala Thr Thr Thr Ala
            180                 185                 190

Ser Leu Ser Asn Gly His Leu Ser Ser Pro Arg Ser Pro Phe Ala Pro
        195                 200                 205

Ala Ala Ala Arg Asp His Leu Phe Asp Lys Thr Val Thr Pro Ser Asp
    210                 215                 220

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys
225                 230                 235                 240

His Phe Pro Leu Gln Leu Pro Ser Ala Gly Gly Glu Ser Lys Gly Val
                245                 250                 255

Leu Leu Asn Phe Glu Asp Ala Ala Gly Lys Val Trp Arg Phe Arg Tyr
            260                 265                 270
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Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
        275                 280                 285


Arg Phe Val Lys Glu Lys Gly Leu His Ala Asp Gly Lys Leu Phe Ile
    290                 295                 300


Asp Cys Lys Leu Val Arg Ser Thr Gly Ala Ala Leu Ala Ser Pro Ala
305                 310                 315                 320


Asp Gln Pro Ala Pro Ser Pro Val Lys Ala Val Arg Leu Phe Gly Val
                325                 330                 335


Asp Leu Leu Thr Ala Pro Ala Pro Val Glu Gln Met Ala Gly Cys Lys
            340                 345                 350


Arg Ala Arg Asp Leu Ala Ala Thr Thr Pro Pro Gln Ala Ala Ala Phe
        355                 360                 365


Lys Lys Gln Cys Ile Glu Leu Ala Leu Val
    370                 375


<210>  37
<211>  1290
<212>  DNA
<213>  Zea mays

<220>
<223> G3432  Predicted polypeptide sequence is orthologous to G867, G9, G993,
 G1930

<400>  37
ctatagctag cactagcagt ggtgcacact gaaatggaca gcgccagcag cctcgtggac      60

gacaccagta gcggtggcgg cggcggcgcg tccacggaca agctaagggc tctggccgtc     120

ttcgccgccg cctcggggac gccgctggag cgcatgggca gcggcgccag cgcggtcgtg     180

gacgcggccg agccgggcgc cgaggcggac tccggttccg gtgccgccgc ggtgagcgtc     240

ggcgggaagc tgccgtcgtc aaggtacaag ggcgtggtgc cgcagcccaa cgggcggtgg     300

ggcgcgcaga tctacgagcg ccaccagcgc gtgtggctcg gcaccttcgc gggcgaggcc     360

gacgcggcgc gcgcctacga cgtcgcggcg cagcggttcc gcggccgcga cgcggtcacc     420

aacttccgcc cgctcgcgga cgccgacccg gacgccgccg ccgagctccg gttcctggcg     480

tcccgctcca aggccgaggt cgtcgacatg ctccgcaagc acacctactt cgacgagctc     540

gcgcagaaca agcgcgcctt cgccgccgcg tccgcgtccg cggccaccgc ctcgtcgctg     600

gccaacaacc cttcttccta cgcgtcgctc tcccccgcga ccgcgacggc cgccgcgcgg     660

gagcacctct tcgacaagac ggtcaccccc agcgacgtgg gcaagctgaa ccggctggtg     720

atcccgaagc agcacgccga gaagcacttc ccgctgcagc tcccatccgc cggcggcgag     780
```

```
agcaagggcg tgctcctcaa cctggaggac gccgcgggca aggtgtggcg gttccgctac     840

tcgtactgga acagcagcca gagctacgtg ctcaccaagg gctggagccg cttcgtcaag     900

gagaagggcc tccaagccgg cgacgtcgtc ggcttctacc gctccgctgc cggcgccgac     960

accaagctct tcatcgactg caagctgcgg cccaacagcg tcgtcgtcgc ctcgacggca    1020

ggcccgtcgc ctccggcgcc ggtggcgaag gccgtgcgtc tcttcggcgt cgacctgctg    1080

acggcaccgg ccaccgccgc ggcgccggcg gaggccgtgg ccgggtgcaa gagagccagg    1140

gacttgggtt cgcccccgca ggcggcgttc aagaagcagc tcgtggagct ggcactagtg    1200

tagattaatg ctacggagcg atcgatcttt ccctggctag ctagtctttt tttttttgc     1260

tcgatcgctc aactcagatg gtagcatcat                                     1290


<210>  38
<211>  389
<212>  PRT
<213>  Zea mays

<220>
<223> G3432 polypeptide Orthologous to G867, G9, G993, G1930

<400>  38

Met Asp Ser Ala Ser Ser Leu Val Asp Asp Thr Ser Ser Gly Gly Gly
1               5                   10                  15


Gly Gly Ala Ser Thr Asp Lys Leu Arg Ala Leu Ala Val Phe Ala Ala
            20                  25                  30


Ala Ser Gly Thr Pro Leu Glu Arg Met Gly Ser Gly Ala Ser Ala Val
        35                  40                  45


Val Asp Ala Ala Glu Pro Gly Ala Glu Ala Asp Ser Gly Ser Gly Ala
    50                  55                  60


Ala Ala Val Ser Val Gly Gly Lys Leu Pro Ser Ser Arg Tyr Lys Gly
65                  70                  75                  80


Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Arg
                85                  90                  95


His Gln Arg Val Trp Leu Gly Thr Phe Ala Gly Glu Ala Asp Ala Ala
            100                 105                 110


Arg Ala Tyr Asp Val Ala Ala Gln Arg Phe Arg Gly Arg Asp Ala Val
        115                 120                 125


Thr Asn Phe Arg Pro Leu Ala Asp Ala Asp Pro Asp Ala Ala Ala Glu
```

```
    130                 135                 140


Leu Arg Phe Leu Ala Ser Arg Ser Lys Ala Glu Val Val Asp Met Leu
145                 150                 155                 160


Arg Lys His Thr Tyr Phe Asp Glu Leu Ala Gln Asn Lys Arg Ala Phe
                165                 170                 175


Ala Ala Ala Ser Ala Ser Ala Ala Thr Ala Ser Ser Leu Ala Asn Asn
            180                 185                 190


Pro Ser Ser Tyr Ala Ser Leu Ser Pro Ala Thr Ala Thr Ala Ala Ala
        195                 200                 205


Arg Glu His Leu Phe Asp Lys Thr Val Thr Pro Ser Asp Val Gly Lys
    210                 215                 220


Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro
225                 230                 235                 240


Leu Gln Leu Pro Ser Ala Gly Gly Glu Ser Lys Gly Val Leu Leu Asn
                245                 250                 255


Leu Glu Asp Ala Ala Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp
            260                 265                 270


Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val
        275                 280                 285


Lys Glu Lys Gly Leu Gln Ala Gly Asp Val Val Gly Phe Tyr Arg Ser
    290                 295                 300


Ala Ala Gly Ala Asp Thr Lys Leu Phe Ile Asp Cys Lys Leu Arg Pro
305                 310                 315                 320


Asn Ser Val Val Val Ala Ser Thr Ala Gly Pro Ser Pro Pro Ala Pro
                325                 330                 335


Val Ala Lys Ala Val Arg Leu Phe Gly Val Asp Leu Leu Thr Ala Pro
            340                 345                 350


Ala Thr Ala Ala Ala Pro Ala Glu Ala Val Ala Gly Cys Lys Arg Ala
        355                 360                 365


Arg Asp Leu Gly Ser Pro Pro Gln Ala Ala Phe Lys Lys Gln Leu Val
    370                 375                 380
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Glu Leu Ala Leu Val
385

<210> 39
<211> 1200
<212> DNA
<213> Zea mays

<220>
<223> G3433 Predicted polypeptide sequence is orthologous to G867, G9, G993, G1930

<400> 39
atggacagcg ccagcagcct cgtggacgac accagcggca gcggcggcgg cgcgtgcacg 60

gacaagctaa gggctttggc cgccgccgcc gcctccgcct cggggccacc gccggagcgc 120

atgggcagcg gagccagcgc ggtcgtggac gcggccgagc cgggcgccga ggcggactcc 180

ggctccgccc cggcctccgt cgccgccgtc gcggcgggcg tgggcgggaa gctgccgtcg 240

tccaggtaca agggcgtggt gccgcagccc aacgggcggt ggggcgcgca gatctacgag 300

cgccacctgc gcgtgtggct cggcaccttc acgggcgagg ccgaggccgc gcgcgcctac 360

gacgtggccg cgcagcggtt ccgggggcgc gacgccgtca ccaacttccg cccgctcgcg 420

gagtcggact tggacccgga cgccgccgcc gagctccggt tcctcgcgtc ccggtccaag 480

gccgaggtcg tcgacatgct ccgcaagcac acctacggcg aggagctcgc gcagaacagg 540

cgcgccttcg ccgctgcggc ggcgtccctg gcctcgccgc agctgccgcc ggccaagaac 600

actagcccgg cggcggcgcg cgagcacatg ttcgacaagg tgctgacccc gagcgacgta 660

ggcaagctca accggctggt ggtgccaaag cagcacgcgg agcggttctt cccggcggcc 720

ggcgccgggt cgacgcagct gtgcttccag gaccgcggcg gggcgctgtg gcagttccgc 780

tactcctact gggggagcag ccagagctat gtcatgacca aggggtggag ccgcttcgtc 840

cgcgccgcac gacttgccgc gggggacacc gtcaccttct cccgcagcgg cggcggccga 900

tacttcatcg agtaccgcca ctgccagcgc cggcgccgcg acgtcgatat cagcttcggc 960

gacgctgcca ccgtgccggc gtggccgagg ccgatagtta tcggaaccgc ggccatgaat 1020

aatgggggtg caacggtggc gtccgccacc atcgccggcc atgacatcga ggtggcagtg 1080

gcaccctcgg gggcgaggag cttcaggctc ttcgggttca atgttgagtg cagcggcgac 1140

gatgcaccgg caccggcacc tgctcccgcc gaagtggagt atgtcgacgg cgacacctag 1200

<210> 40
<211> 399
<212> PRT
<213> Zea mays

<220>
<223> G3433 polypeptide Orthologous to G867, G9, G993, G1930

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<400>  40

Met Asp Ser Ala Ser Ser Leu Val Asp Asp Thr Ser Gly Ser Gly Gly
1               5                   10                  15


Gly Ala Cys Thr Asp Lys Leu Arg Ala Leu Ala Ala Ala Ala Ala Ser
            20                  25                  30


Ala Ser Gly Pro Pro Pro Glu Arg Met Gly Ser Gly Ala Ser Ala Val
        35                  40                  45


Val Asp Ala Ala Glu Pro Gly Ala Glu Ala Asp Ser Gly Ser Ala Pro
    50                  55                  60


Ala Ser Val Ala Ala Val Ala Ala Gly Val Gly Gly Lys Leu Pro Ser
65                  70                  75                  80


Ser Arg Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala
                85                  90                  95


Gln Ile Tyr Glu Arg His Leu Arg Val Trp Leu Gly Thr Phe Thr Gly
            100                 105                 110


Glu Ala Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala Gln Arg Phe Arg
        115                 120                 125


Gly Arg Asp Ala Val Thr Asn Phe Arg Pro Leu Ala Glu Ser Asp Leu
    130                 135                 140


Asp Pro Asp Ala Ala Ala Glu Leu Arg Phe Leu Ala Ser Arg Ser Lys
145                 150                 155                 160


Ala Glu Val Val Asp Met Leu Arg Lys His Thr Tyr Gly Glu Glu Leu
                165                 170                 175


Ala Gln Asn Arg Arg Ala Phe Ala Ala Ala Ala Ser Leu Ala Ser
            180                 185                 190


Pro Gln Leu Pro Pro Ala Lys Asn Thr Ser Pro Ala Ala Ala Arg Glu
        195                 200                 205


His Met Phe Asp Lys Val Leu Thr Pro Ser Asp Val Gly Lys Leu Asn
    210                 215                 220


Arg Leu Val Val Pro Lys Gln His Ala Glu Arg Phe Phe Pro Ala Ala
225                 230                 235                 240


Gly Ala Gly Ser Thr Gln Leu Cys Phe Gln Asp Arg Gly Gly Ala Leu
```

```
                245                 250                 255

Trp Gln Phe Arg Tyr Ser Tyr Trp Gly Ser Ser Gln Ser Tyr Val Met
            260                 265                 270

Thr Lys Gly Trp Ser Arg Phe Val Arg Ala Ala Arg Leu Ala Ala Gly
        275                 280                 285

Asp Thr Val Thr Phe Ser Arg Ser Gly Gly Gly Arg Tyr Phe Ile Glu
    290                 295                 300

Tyr Arg His Cys Gln Arg Arg Arg Arg Asp Val Asp Ile Ser Phe Gly
305                 310                 315                 320

Asp Ala Ala Thr Val Pro Ala Trp Pro Arg Pro Ile Val Ile Gly Thr
                325                 330                 335

Ala Ala Met Asn Asn Gly Gly Ala Thr Val Ala Ser Ala Thr Ile Ala
            340                 345                 350

Gly His Asp Ile Glu Val Ala Val Ala Pro Ser Gly Ala Arg Ser Phe
        355                 360                 365

Arg Leu Phe Gly Phe Asn Val Glu Cys Ser Gly Asp Asp Ala Pro Ala
    370                 375                 380

Pro Ala Pro Ala Pro Ala Glu Val Glu Tyr Val Asp Gly Asp Thr
385                 390                 395


<210>  41
<211>  969
<212>  DNA
<213>  Brassica oleraceae

<220>
<223> BZ458719  Predicted sequence is orthologous to G867, G9, G993, G1930

<400>  41
caacccggcc cgtatcctgt tccaacccag cctttgtact tccacacaat atacaactgt      60

tgatcctgac cgttagatct tttaaaactg atcaaatcac cggcacagag tctcttctct     120

ttaacgaacc tgctccaacc tttagtcaac acgtagcttt gactactgtt ccaatacgag     180

taacggaacc tccacacttt cccgttaacg tcttcgaaat tcaacagcgt ccctctcacg     240

gagacgtcgc cggttaacgg taacggaaaa tgtttctccg cttggtgttt cggtatcact     300

aaacggttta gcttcccgac gtcactcggc gttaccgttt tctcaaacag acactccgcc     360

gttttaaacc ccgtcacaac cgtaacgtta gcaaacgccg tctcttccgt gtctccgtta     420

ccaccgttac gtttgcgttt cctctgctct aactcttctt tgtaagtgtg tttcctcaac     480
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atatcaacga tctcatattt cgaatgtgcg tttaagaact ttacttcgtc tccgtcacct     540

tcaccgttac ggaacgtcgt gtctggtttg aaattagtga cggcgtcaga gccgcggaaa     600

cggtgagcgg cgacgtcgta gacacgcgcc gcttcttctt cttcgttgaa tgtcccgagc     660

caaacgcgct tgtgcttctc gtatatctga gctccccatc ttccgtttgg ctgagggacg     720

acgcctttga attttgacga cgggagcttt cttgattctg cttcgacgcc gttctgggaa     780

tcgagaacca cgcttgaacc gcttcccatt ctgtataaac tcgccggaga tgacgacttc     840

gccgtcttcg gcggcggtgt atcttagccg gagtgtggat ggaaactgta cttgttgagc     900

tctccatcac actactcaca gctttcatat tagagaaatc acaagaaagt tgtgaaattt     960

gagaatgaa                                                              969


<210>  42
<211>  288
<212>  PRT
<213>  Brassica oleraceae


<220>
<221>  misc_feature
<222>  (288)..(288)
<223>  Xaa can be any naturally occurring amino acid

<220>
<223> BZ458719 polypeptide Orthologous to G867, G9, G993, G1930

<400>  42

Asp Thr Pro Pro Pro Lys Thr Ala Lys Ser Ser Ser Pro Ala Ser Leu
1               5                   10                  15


Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Gln Asn Gly
            20                  25                  30


Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Phe Lys Gly Val
        35                  40                  45


Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His
    50                  55                  60


Lys Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Arg
65                  70                  75                  80


Val Tyr Asp Val Ala Ala His Arg Phe Arg Gly Ser Asp Ala Val Thr
                85                  90                  95


Asn Phe Lys Pro Asp Thr Thr Phe Arg Asn Gly Glu Gly Asp Gly Asp
            100                 105                 110
```

```
Glu Val Lys Phe Leu Asn Ala His Ser Lys Tyr Glu Ile Val Asp Met
        115                 120                 125


Leu Arg Lys His Thr Tyr Lys Glu Glu Leu Glu Gln Arg Lys Arg Lys
    130                 135                 140


Arg Asn Gly Gly Asn Gly Asp Thr Glu Glu Thr Ala Phe Ala Asn Val
145                 150                 155                 160


Thr Val Val Thr Gly Phe Lys Thr Ala Glu Cys Leu Phe Glu Lys Thr
                165                 170                 175


Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys
            180                 185                 190


His Gln Ala Glu Lys His Phe Pro Leu Pro Leu Thr Gly Asp Val Ser
        195                 200                 205


Val Arg Gly Thr Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp
    210                 215                 220


Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr
225                 230                 235                 240


Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp
                245                 250                 255


Leu Ile Ser Phe Lys Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile
            260                 265                 270


Val Trp Lys Tyr Lys Gly Trp Val Gly Thr Gly Tyr Gly Pro Gly Xaa
        275                 280                 285


<210>  43
<211>  756
<212>  DNA
<213>  Helianthus annuus

<220>
<223> BQ971511  Predicted sequence is orthologous to G867, G9, G993, G1930

<400>  43
ttggaagcgg agccagcgtg gtttctgacc cggaagtgga agccttgtcg aggaagctac      60

cgtcgtcgag atataaaggc gttgttccgc aagcgaatgg ccgttgggga gctcagattt     120

atgagaaaca tcaaagggta tggcttggca cgtttaacga cgaagacgaa gccgcgaaag     180

cgtacgacgt cgcggtccaa cgctttcgcg gacgagacgc agtaacaaac ttcaagcaac     240

tcgtcaccga cgacaacgcc gctgcctttg aagcaacttt cttaaaccgt cactcaaaat     300
```

```
ccgaaatagt tgacatgcta agaaaacaca catacaatga cgagttagaa caaagcaaaa     360

gaaccatcaa cacacacaaa accctatttc aaaccgggtt caaccttccc ggaccgggtt     420

gcaccatgcc acgcgaacac ctcttccaaa aaaccgtcac accaagcgac gttggcaaac     480

taaaccggct cgtgatacca aaacaacatg ctgaaaaaca ctttccggtt caaaaaggca     540

tcagttcaaa gggagttttg ttacacttcg aagataccga gtcaaaagtt tggcgatttc     600

ggtattcata ttggaatagt agccagagtt atgtgttaac caaagggtgg agccggtttg     660

ttaaagaaaa gaaccttaaa gccggtgata gcgttagctt tcacagctcg accggaacgg     720

ataagcagtt ttacattcac tgggagtcaa aaaccg                               756


<210>  44
<211>  252
<212>  PRT
<213>  Helianthus annuus


<220>
<221>  misc_feature
<222>  (252)..(252)
<223>  Xaa can be any naturally occurring amino acid

<220>
<223> BQ971511 polypeptide Orthologous to G867, G9, G993, G1930

<400>  44

Gly Ser Gly Ala Ser Val Val Ser Asp Pro Glu Val Glu Ala Leu Ser
1               5                   10                  15


Arg Lys Leu Pro Ser Ser Arg Tyr Lys Gly Val Val Pro Gln Ala Asn
            20                  25                  30


Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu
        35                  40                  45


Gly Thr Phe Asn Asp Glu Asp Glu Ala Ala Lys Ala Tyr Asp Val Ala
    50                  55                  60


Val Gln Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Gln Leu
65                  70                  75                  80


Val Thr Asp Asp Asn Ala Ala Ala Phe Glu Ala Thr Phe Leu Asn Arg
                85                  90                  95


His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Asn
            100                 105                 110


Asp Glu Leu Glu Gln Ser Lys Arg Thr Ile Asn Thr His Lys Thr Leu
```

```
        115                 120                 125


Phe Gln Thr Gly Phe Asn Leu Pro Gly Pro Gly Cys Thr Met Pro Arg
    130                 135                 140


Glu His Leu Phe Gln Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu
145                 150                 155                 160


Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Val
                165                 170                 175


Gln Lys Gly Ile Ser Ser Lys Gly Val Leu Leu His Phe Glu Asp Thr
            180                 185                 190


Glu Ser Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln
        195                 200                 205


Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn
    210                 215                 220


Leu Lys Ala Gly Asp Ser Val Ser Phe His Ser Ser Thr Gly Thr Asp
225                 230                 235                 240


Lys Gln Phe Tyr Ile His Trp Glu Ser Lys Thr Xaa
                245                 250


<210>  45
<211>  743
<212>  DNA
<213>  Helianthus annuus

<220>
<223> BU025988  Predicted sequence is orthologous to G867, G9, G993, G1930

<400>  45
ttggaagcgg atccagcgtg gttcttgacc cagaaggagg cgtggaagtt gaagctcagt     60

cgagaaagct accctcgtcg cgatacaaag gtgtcgttcc acaaccgaat ggccgttggg    120

gagctcagat ttacgagaaa caccaaaggg tatggttagg tacgttcaac gacgaagatg    180

aagctgcaaa ggcgtacgat gttgccgtac aacgcttccg cggccgagac gcggtcacaa    240

acattaagca ggttgatgcc gacgataaag aggccgcgat ggaagcaagt ttcttaagcc    300

gccattcgga gtcagaaatt gttgacatgc ttagaaaaca cacatacaat gacgagctag    360

aacaaagcaa aagaagctgc acctcacacc aaaccctttc tcaaaccggt ttaaccaaca    420

ccacccgttt agtctccatg aagccacgcg aacacctctt ccagaaaacc gtgaccccta    480

gcgacgtagg aaagctgaac cggctcgtta taccaaaaca acacgcggag aaacacttcc    540

cggttcaaaa agggagcaat tcaaaaggag ttcttttaca tttcgaagat aaagggtcaa    600
```

```
aagtatggag atttcgttac tcttactgga acagtagcca gagttatgtt ttaaccaaag      660

gctggagccg gttcgtgaaa gaaaaaaatc taaaagccgg agatagcgtc agctttcaaa      720

gctcaaccgg accggataag cag                                              743


<210>  46
<211>  247
<212>  PRT
<213>  Helianthus annuus

<220>
<223>  BU025988 polypeptide Orthologous to G867, G9, G993, G1930

<400>  46

Gly Ser Gly Ser Ser Val Val Leu Asp Pro Glu Gly Gly Val Glu Val
1               5                   10                  15


Glu Ala Gln Ser Arg Lys Leu Pro Ser Ser Arg Tyr Lys Gly Val Val
            20                  25                  30


Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln
        35                  40                  45


Arg Val Trp Leu Gly Thr Phe Asn Asp Glu Asp Glu Ala Ala Lys Ala
    50                  55                  60


Tyr Asp Val Ala Val Gln Arg Phe Arg Gly Arg Asp Ala Val Thr Asn
65                  70                  75                  80


Ile Lys Gln Val Asp Ala Asp Asp Lys Glu Ala Ala Met Glu Ala Ser
                85                  90                  95


Phe Leu Ser Arg His Ser Glu Ser Glu Ile Val Asp Met Leu Arg Lys
            100                 105                 110


His Thr Tyr Asn Asp Glu Leu Glu Gln Ser Lys Arg Ser Cys Thr Ser
        115                 120                 125


His Gln Thr Leu Ser Gln Thr Gly Leu Thr Asn Thr Thr Arg Leu Val
    130                 135                 140


Ser Met Lys Pro Arg Glu His Leu Phe Gln Lys Thr Val Thr Pro Ser
145                 150                 155                 160


Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu
                165                 170                 175


Lys His Phe Pro Val Gln Lys Gly Ser Asn Ser Lys Gly Val Leu Leu
```

```
            180                 185                 190


His Phe Glu Asp Lys Gly Ser Lys Val Trp Arg Phe Arg Tyr Ser Tyr
        195                 200                 205


Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe
    210                 215                 220


Val Lys Glu Lys Asn Leu Lys Ala Gly Asp Ser Val Ser Phe Gln Ser
225                 230                 235                 240


Ser Thr Gly Pro Asp Lys Gln
                245


<210>  47
<211>  1470
<212>  DNA
<213>  Triticum aestivum

<220>
<223> BT009310 Predicted sequence is orthologous to G867, G9, G993, G1930

<400>  47
gcacgaggct agcttcagct tttagctaag ctctacttcc ctcccgagct aagcatcttc      60

ttgatttctc ggtgatcgga ttcggatgga cagcgcaaga agctgcctcg tggacgacgt     120

gagcagcggc gcgtccacgg gcaagaaggc ctctccgtcc ccggccgcgc cggcgaccaa     180

gccgctgcag cgcgtgggca gcggggccag cgcggtcatg gacgcgccgg agcccggcgc     240

cgaggcggac tccggccgcg tcggcaggct gccgtcctcc aagtacaagg gcgtggtgcc     300

gcagcccaac gggcgctggg gcgcgcagat ctacgagcgc caccagcgcg tctggctcgg     360

caccttcacg gggagggccg aggctgcgcg cgcctacgac gcggcggcgc agcgcttccg     420

cggccgcgac gcagtcacca acttccgccc gctcaccgag tccgacccgg aggacgccgc     480

cgagctccgc ttcctcgctg cccgctccaa ggccgaggtc gtcgacatgc tgcgcaagca     540

cacctatccc gacgagctcg ctcagtacaa gcgcgcctac ttcgccgccg ctgcggcgtc     600

ctcccctaca tcgtcctcgg tgcctcccgc ctcgtcgccc tcttcggcgg cttcgccctc     660

gccggcggcg cggcgcgagc acctgttcga caagacggtc acgcccagcg acgtggggaa     720

gctgaaccgg cttgtgatac cgaagcagca cgccgagaag cactttcctc tccagcttcc     780

ttccgccggc gccgccgtgt ccggcgagtg caagggcatg cttctcaact tcgacgactc     840

ggccggcaag gtgtggaggt tccggtactc gtactggaac agcagccaga gctacgtgct     900

caccaagggc tggagccgct ttgtcaagga gaagggcctg cacgccggcg acgccgtcgg     960

gttctaccgc tctgcctcag gcagcaacca gctcttcatc gactgcaagc tccggtccaa    1020

gaccacgacg atgacgacga ctttcgtcaa cgcggcggcc gccccgtcgc cggcacccgt    1080
```

```
gatgaggacc gtgcgactct tcggcgtcga ccttctcacg gcgccggcgc cgagtcacgc    1140

gcccgagcac gaggactgca gcatggtgcc caagacaagc aagagatcca tggacgccaa    1200

cgcagcggcc actccggcgc acgcggtctg gaagaagcgg tgcatagact tcgcgctgac    1260

ctagccagct agcgtttttc ctccatggtt gctttgcttg cctccaaatt tccatgttag    1320

tagcttagag ctcttgatcg gtccaagtgt ttgccttttt tttcctcttc ttctcataca    1380

caagttagct ctaaatccag tcttctttaa ttaatctact gtaaattaag cccgttctcg    1440

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                                     1470
```

<210> 48
<211> 392
<212> PRT
<213> Triticum aestivum

<220>
<223> BT009310 polypeptide Orthologous to G867, G9, G993, G1930

<400> 48

```
Met Asp Ser Ala Arg Ser Cys Leu Val Asp Asp Val Ser Ser Gly Ala
1               5                   10                  15


Ser Thr Gly Lys Lys Ala Ser Pro Ser Pro Ala Ala Pro Ala Thr Lys
            20                  25                  30


Pro Leu Gln Arg Val Gly Ser Gly Ala Ser Ala Val Met Asp Ala Pro
        35                  40                  45


Glu Pro Gly Ala Glu Ala Asp Ser Gly Arg Val Gly Arg Leu Pro Ser
    50                  55                  60


Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala
65                  70                  75                  80


Gln Ile Tyr Glu Arg His Gln Arg Val Trp Leu Gly Thr Phe Thr Gly
                85                  90                  95


Glu Ala Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Gln Arg Phe Arg
            100                 105                 110


Gly Arg Asp Ala Val Thr Asn Phe Arg Pro Leu Thr Glu Ser Asp Pro
        115                 120                 125


Glu Asp Ala Ala Glu Leu Arg Phe Leu Ala Ala Arg Ser Lys Ala Glu
    130                 135                 140


Val Val Asp Met Leu Arg Lys His Thr Tyr Pro Asp Glu Leu Ala Gln
```

```
145                 150                 155                 160

Tyr Lys Arg Ala Tyr Phe Ala Ala Ala Ala Ala Ser Ser Pro Thr Ser
                165                 170                 175

Ser Ser Val Pro Pro Ala Ser Ser Pro Ser Ser Ala Ala Ser Pro Ser
            180                 185                 190

Pro Ala Ala Arg Arg Glu His Leu Phe Asp Lys Thr Val Thr Pro Ser
        195                 200                 205

Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu
    210                 215                 220

Lys His Phe Pro Leu Gln Leu Pro Ser Ala Gly Ala Ala Val Ser Gly
225                 230                 235                 240

Glu Cys Lys Gly Met Leu Leu Asn Phe Asp Asp Ser Ala Gly Lys Val
                245                 250                 255

Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu
            260                 265                 270

Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Gly Leu His Ala Gly
        275                 280                 285

Asp Ala Val Gly Phe Tyr Arg Ser Ala Ser Gly Ser Asn Gln Leu Phe
    290                 295                 300

Ile Asp Cys Lys Leu Arg Ser Lys Thr Thr Thr Met Thr Thr Thr Phe
305                 310                 315                 320

Val Asn Ala Ala Ala Ala Pro Ser Pro Ala Pro Val Met Arg Thr Val
                325                 330                 335

Arg Leu Phe Gly Val Asp Leu Leu Thr Ala Pro Ala Pro Ser His Ala
            340                 345                 350

Pro Glu His Glu Asp Cys Ser Met Val Pro Lys Thr Ser Lys Arg Ser
        355                 360                 365

Met Asp Ala Asn Ala Ala Ala Thr Pro Ala His Ala Val Trp Lys Lys
    370                 375                 380

Arg Cys Ile Asp Phe Ala Leu Thr
385                 390
```

```
<210>  49
<211>  914
<212>  DNA
<213>  Zea mays

<220>
<223> CC616336  Predicted sequence is orthologous to G867, G9, G993, G1930

<400>  49
gaagagctgc tgcttgccgc cggcggaacg gtagaacccg acggcgtcgc cggcgtggag      60

cccccttctcc ttgacgaagc ggctccaccc cttggtcagc acgtagctct ggctgctgtt    120

ccagtacgag taccggaacc tccacgcctt cccggcggcg tcctcgaagt tgaggagcac     180

gcccttgcac tcgccgccac taccgacgcc cgccgccgcc gccgccggga gctgcagcgg     240

gaagtgcttc tccgcgtgct gcttcggtat caccagccgg ttcagcttcc ccacgtcgct     300

cggcgtcacc gtcttgtcga agaggtgctc gcgcgccgcc gcgggcgacg acgacgacga     360

ggcggcgggc ggacggcggt tattctcggg cggcggcgag gcggccgggg acgccgcggc     420

gaaggcgcgc ctgttgtgcg cgagctcctc gccgtaggtg tgcttgcgga gcatgtcgac     480

gacctcggcc ttggaccggg acgcgaggaa ccggagctcg acggcggcct ccggctccga     540

ctccgccagc gggcggaagt tggtgacggc gtcgcggccc cggaaccgct gcgcggccac     600

gtcgtaggcg cgcgcggcct cggcctcgcc cgtgaacgtg ccgagccaca cgcgctggtg     660

ccgctcgtag atctgcgcgc cccaccgccc gttgggctgt ggcaccacgc ccttgtactt     720

ggacgacggc agcttcccgc tgaccccgcc gggggcccgc cccgcgccgc ccgagtctgc     780

ctcggcgccc ggctccgccg cgtccatcac cgcgctggtg ccgctgccca cgcgctgtag     840

cggcttgccg gtcgccgcag ccggagccgg cgccggtttc ttgcccgtgg acgcgccgct     900

gctcgcgtcg tcca                                                       914


<210>  50
<211>  304
<212>  PRT
<213>  Zea mays

<220>
<223> CC616336 polypeptide Orthologous to G867, G9, G993, G1930

<400>  50

Asp Asp Ala Ser Ser Gly Ala Ser Thr Gly Lys Lys Pro Ala Pro Ala
1               5                   10                  15


Pro Ala Ala Ala Thr Gly Lys Pro Leu Gln Arg Val Gly Ser Gly Thr
            20                  25                  30


Ser Ala Val Met Asp Ala Ala Glu Pro Gly Ala Glu Ala Asp Ser Gly
        35                  40                  45
```

```
Gly Ala Gly Arg Ala Pro Gly Gly Val Ser Gly Lys Leu Pro Ser Ser
    50                  55                  60

Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln
65                  70                  75                  80

Ile Tyr Glu Arg His Gln Arg Val Trp Leu Gly Thr Phe Thr Gly Glu
                85                  90                  95

Ala Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala Gln Arg Phe Arg Gly
            100                 105                 110

Arg Asp Ala Val Thr Asn Phe Arg Pro Leu Ala Glu Ser Glu Pro Glu
        115                 120                 125

Ala Ala Val Glu Leu Arg Phe Leu Ala Ser Arg Ser Lys Ala Glu Val
    130                 135                 140

Val Asp Met Leu Arg Lys His Thr Tyr Gly Glu Glu Leu Ala His Asn
145                 150                 155                 160

Arg Arg Ala Phe Ala Ala Ala Ser Pro Ala Ala Ser Pro Pro Pro Glu
                165                 170                 175

Asn Asn Arg Arg Pro Pro Ala Ala Ser Ser Ser Ser Ser Pro Ala Ala
            180                 185                 190

Ala Arg Glu His Leu Phe Asp Lys Thr Val Thr Pro Ser Asp Val Gly
        195                 200                 205

Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe
    210                 215                 220

Pro Leu Gln Leu Pro Ala Ala Ala Ala Ala Gly Val Gly Ser Gly Gly
225                 230                 235                 240

Glu Cys Lys Gly Val Leu Leu Asn Phe Glu Asp Ala Ala Gly Lys Ala
                245                 250                 255

Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu
            260                 265                 270

Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Gly Leu His Ala Gly
        275                 280                 285

Asp Ala Val Gly Phe Tyr Arg Ser Ala Gly Gly Lys Gln Gln Leu Phe
    290                 295                 300
```

```
<210>  51
<211>  1182
<212>  DNA
<213>  Oryza sativa

<220>
<223> AAAA01000997  Predicted sequence is orthologous to G867, G9, G993, G193
0

<400>  51
atggacagca cgagctgtct cttggacgac gcgagcagcg gcgcgtccac gggcaagaag     60

gcggcggcgg cggcggcgtc gaaggcgctg cagcgcgtgg gcagcggcgc cagcgcggtg    120

atggacgcgg ccgagcctgg cgccgaggcg gactcgggcg gcgagcggcg cggcggcggc    180

ggcgggaagc tgccgtcgtc caagtacaag ggcgtggtgc cgcaaccgaa cgggcggtgg    240

ggcgcgcaga tatacgagcg gcaccagcgg gtgtggctcg gcacgttcac cggcgaggcg    300

gaggcggcgc gcgcctacga cgtggcggcg cagcggttcc gcggccgcga cgccgtcacc    360

aacttccgcc cgctcgccga gtccgacccg gaggccgctg tcgagctccg cttcctcgcg    420

tcccgctcca aggccgaggt cgtcgacatg ctccgcaagc acacctacct cgaggagctc    480

acgcagaaca agcgcgcctt cgccgccatc tccccgccgc cccccaagca ccccgcctcc    540

tctccgccgt cctccgccgc cgcgcgcgag cacctgttcg acaagacggt gacgcccagc    600

gacgtcggga agctgaaccg gctggtgatc cccaagcagc acgccgagaa gcacttcccg    660

ctccagctcc ctccccctac cacaacctcc tccgtcgccg ccgccgccga cgccgccgcc    720

ggcggcggcg agtgcaaggg agtcctcctc aacttcgagg acgccgccgg gaaggtgtgg    780

aaattccggt actcctactg gaacagcagc cagagctacg tgctcaccaa ggggtggagc    840

cgcttcgtca aggacaaggg gctccacgcc ggcgacgccg tcggcttcta ccgcgccgcc    900

ggtaagaacg cgcagctctt catcgactgc aaggtccggg caaaacccac caccgccgcc    960

gccgccgccg ccttcctcag cgcggtggcc gccgccgccg cgccgccacc cgccgtgaag   1020

gctatcaggc tgttcggtgt cgacctgctc acggcggcgg cgccggagct gcaggacgcc   1080

ggcggcgccg ccatgaccaa gagcaagaga gccatggacg ccatggctga gtcacaagcg   1140

cacgtggttt ttaagaagca atgcatagag ctcgcgctaa cc                      1182


<210>  52
<211>  394
<212>  PRT
<213>  Oryza sativa

<220>
<223> AAAA01000997 polypeptide Orthologous to G867, G9, G993, G1930

<400>  52
```

```
Met Asp Ser Thr Ser Cys Leu Leu Asp Asp Ala Ser Ser Gly Ala Ser
1               5                   10                  15

Thr Gly Lys Lys Ala Ala Ala Ala Ala Ala Ser Lys Ala Leu Gln Arg
            20                  25                  30

Val Gly Ser Gly Ala Ser Ala Val Met Asp Ala Ala Glu Pro Gly Ala
        35                  40                  45

Glu Ala Asp Ser Gly Gly Glu Arg Arg Gly Gly Gly Gly Gly Lys Leu
    50                  55                  60

Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp
65                  70                  75                  80

Gly Ala Gln Ile Tyr Glu Arg His Gln Arg Val Trp Leu Gly Thr Phe
                85                  90                  95

Thr Gly Glu Ala Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala Gln Arg
            100                 105                 110

Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Arg Pro Leu Ala Glu Ser
        115                 120                 125

Asp Pro Glu Ala Ala Val Glu Leu Arg Phe Leu Ala Ser Arg Ser Lys
    130                 135                 140

Ala Glu Val Val Asp Met Leu Arg Lys His Thr Tyr Leu Glu Glu Leu
145                 150                 155                 160

Thr Gln Asn Lys Arg Ala Phe Ala Ala Ile Ser Pro Pro Pro Pro Lys
                165                 170                 175

His Pro Ala Ser Ser Pro Pro Ser Ser Ala Ala Ala Arg Glu His Leu
            180                 185                 190

Phe Asp Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
        195                 200                 205

Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Gln Leu Pro
    210                 215                 220

Pro Pro Thr Thr Thr Ser Ser Val Ala Ala Ala Ala Asp Ala Ala Ala
225                 230                 235                 240

Gly Gly Gly Glu Cys Lys Gly Val Leu Leu Asn Phe Glu Asp Ala Ala
                245                 250                 255
```

```
Gly Lys Val Trp Lys Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
            260                 265                 270

Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Asp Lys Gly Leu
        275                 280                 285

His Ala Gly Asp Ala Val Gly Phe Tyr Arg Ala Ala Gly Lys Asn Ala
    290                 295                 300

Gln Leu Phe Ile Asp Cys Lys Val Arg Ala Lys Pro Thr Thr Ala Ala
305                 310                 315                 320

Ala Ala Ala Ala Phe Leu Ser Ala Val Ala Ala Ala Ala Ala Pro Pro
                325                 330                 335

Pro Ala Val Lys Ala Ile Arg Leu Phe Gly Val Asp Leu Leu Thr Ala
            340                 345                 350

Ala Ala Pro Glu Leu Gln Asp Ala Gly Gly Ala Ala Met Thr Lys Ser
        355                 360                 365

Lys Arg Ala Met Asp Ala Met Ala Glu Ser Gln Ala His Val Val Phe
    370                 375                 380

Lys Lys Gln Cys Ile Glu Leu Ala Leu Thr
385                 390


<210>  53
<211>  393
<212>  PRT
<213>  Oryza sativa

<220>
<223> OSC26104.C1.p13.fg polypeptide Orthologous to G867, G9, G993, G1930

<400>  53

Met Asp Ser Ser Ser Cys Leu Val Asp Asp Thr Asn Ser Gly Gly Ser
1               5                   10                  15

Ser Thr Asp Lys Leu Arg Ala Leu Ala Ala Ala Ala Ala Glu Thr Ala
            20                  25                  30

Pro Leu Glu Arg Met Gly Ser Gly Ala Ser Ala Val Val Asp Ala Ala
        35                  40                  45

Glu Pro Gly Ala Glu Ala Asp Ser Gly Ser Gly Gly Arg Val Cys Gly
    50                  55                  60
```

```
Gly Gly Gly Gly Gly Ala Gly Gly Ala Gly Gly Lys Leu Pro Ser Ser
65                  70                  75                  80

Lys Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln
                85                  90                  95

Ile Tyr Glu Arg His Gln Arg Val Trp Leu Gly Thr Phe Ala Gly Glu
            100                 105                 110

Asp Asp Ala Ala Arg Ala Tyr Asp Val Ala Ala Gln Arg Phe Arg Gly
        115                 120                 125

Arg Asp Ala Val Thr Asn Phe Arg Pro Leu Ala Glu Ala Asp Pro Asp
    130                 135                 140

Ala Ala Ala Glu Leu Arg Phe Leu Ala Thr Arg Ser Lys Ala Glu Val
145                 150                 155                 160

Val Asp Met Leu Arg Lys His Thr Tyr Phe Asp Glu Leu Ala Gln Ser
                165                 170                 175

Lys Arg Thr Phe Ala Ala Ser Thr Pro Ser Ala Ala Thr Thr Thr Ala
            180                 185                 190

Ser Leu Ser Asn Gly His Leu Ser Ser Pro Arg Ser Pro Phe Ala Pro
        195                 200                 205

Ala Ala Ala Arg Asp His Leu Phe Asp Lys Thr Val Thr Pro Ser Asp
    210                 215                 220

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys
225                 230                 235                 240

His Phe Pro Leu Gln Leu Pro Ser Ala Gly Gly Glu Ser Lys Gly Val
                245                 250                 255

Leu Leu Asn Phe Glu Asp Ala Ala Gly Lys Val Trp Arg Phe Arg Tyr
            260                 265                 270

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
        275                 280                 285

Arg Phe Val Lys Glu Lys Gly Leu His Ala Gly Asp Val Val Gly Phe
    290                 295                 300

Tyr Arg Ser Ala Ala Ser Ala Gly Asp Asp Gly Lys Leu Phe Ile Asp
305                 310                 315                 320
```

```
Cys Lys Leu Val Arg Ser Thr Gly Ala Ala Leu Ala Ser Pro Ala Asp
                325                 330                 335


Gln Pro Ala Pro Ser Pro Val Lys Ala Val Arg Leu Phe Gly Val Asp
            340                 345                 350


Leu Leu Thr Ala Pro Ala Pro Val Glu Gln Met Ala Gly Cys Lys Arg
        355                 360                 365


Ala Arg Asp Leu Ala Ala Thr Thr Pro Pro Gln Ala Ala Ala Phe Lys
    370                 375                 380


Lys Gln Cys Ile Glu Leu Ala Leu Val
385                 390


<210>  54
<211>  929
<212>  DNA
<213>  Arabidopsis thaliana

<220>
<223> CBF1  G40

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agacagatat actatctttt attaatccaa aaagactgag aactctagta actacgtact     120

acttaaacct tatccagttt cttgaaacag agtactctga tcaatgaact cattttcagc     180

tttttctgaa atgtttggct ccgattacga gcctcaaggc ggagattatt gtccgacgtt     240

ggccacgagt tgtccgaaga aaccggcggg ccgtaagaag tttcgtgaga ctcgtcaccc     300

aatttacaga ggagttcgtc aaagaaactc cggtaagtgg gtttctgaag tgagagagcc     360

aaacaagaaa accaggattt ggctcgggac tttccaaacc gctgagatgg cagctcgtgc     420

tcacgacgtc gctgcattag ccctccgtgg ccgatcagca tgtctcaact tcgctgactc     480

ggcttggcgg ctacgaatcc cggagtcaac atgcgccaag gatatccaaa aagcggctgc     540

tgaagcggcg ttggcttttc aagatgagac gtgtgatacg acgaccacga atcatggcct     600

ggacatggag gagacgatgg tggaagctat ttatacaccg gaacagagcg aaggtgcgtt     660

ttatatggat gaggagacaa tgtttgggat gccgactttg ttggataata tggctgaagg     720

catgctttta ccgccgccgt ctgttcaatg gaatcataat tatgacggcg aaggagatgg     780

tgacgtgtcg ctttggagtt actaatattc gatagtcgtt tccatttttg tactatagtt     840

tgaaaatatt ctagttcctt tttttagaat ggttccttca ttttatttta ttttattgtt     900

gtagaaacga gtggaaaata attcaatac                                      929
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<210>  55
<211>  213
<212>  PRT
<213>  Arabidopsis thaliana

<220>
<223> CBF1 polypeptide G40

<400>  55

Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
1               5                   10                  15


Pro Gln Gly Gly Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys
            20                  25                  30


Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr
        35                  40                  45


Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg
    50                  55                  60


Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala
65                  70                  75                  80


Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly
                85                  90                  95


Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile
            100                 105                 110


Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala
        115                 120                 125


Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Thr Asn His
    130                 135                 140


Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu
145                 150                 155                 160


Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met
                165                 170                 175


Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro
            180                 185                 190


Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val
        195                 200                 205


Ser Leu Trp Ser Tyr
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210

<210> 56
<211> 803
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> CBF2 G41

<400> 56
ctgatcaatg aactcatttt ctgccttttc tgaaatgttt ggctccgatt acgagtctcc 60

ggtttcctca ggcggtgatt acagtccgaa gcttgccacg agctgcccca agaaaccagc 120

gggaaggaag aagtttcgtg agactcgtca cccaatttac agaggagttc gtcaaagaaa 180

ctccggtaag tgggtgtgtg agttgagaga gccaaacaag aaaacgagga tttggctcgg 240

gactttccaa accgctgaga tggcagctcg tgctcacgac gtcgccgcca tagctctccg 300

tggcagatct gcctgtctca atttcgctga ctcggcttgg cggctacgaa tcccggaatc 360

aacctgtgcc aaggaaatcc aaaaggcggc ggctgaagcc gcgttgaatt ttcaagatga 420

gatgtgtcat atgacgacgg atgctcatgg tcttgacatg gaggagacct tggtggaggc 480

tatttatacg ccggaacaga gccaagatgc gttttatatg gatgaagagg cgatgttggg 540

gatgtctagt ttgttggata acatggccga agggatgctt ttaccgtcgc cgtcggttca 600

atggaactat aattttgatg tcgagggaga tgatgacgtg tccttatgga gctattaaaa 660

ttcgattttt atttccattt ttggtattat agctttttat acatttgatc ctttttttaga 720

atggatcttc ttcttttttt ggttgtgaga aacgaatgta aatggtaaaa gttgttgtca 780

aatgcaaatg tttttgagtg cag 803

<210> 57
<211> 207
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> CBF2 polypeptide G41

<400> 57

Met Phe Gly Ser Asp Tyr Glu Ser Pro Val Ser Ser Gly Gly Asp Tyr
1 5 10 15

Ser Pro Lys Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly Arg Lys
20 25 30

Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg
35 40 45

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Asn Ser Gly Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr
    50                  55                  60


Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala
65                  70                  75                  80


His Asp Val Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn
                85                  90                  95


Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala
            100                 105                 110


Lys Glu Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp
        115                 120                 125


Glu Met Cys His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu
    130                 135                 140


Thr Leu Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe
145                 150                 155                 160


Tyr Met Asp Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn
                165                 170                 175


Met Ala Glu Gly Met Leu Leu Pro Ser Pro Ser Val Gln Trp Asn Tyr
            180                 185                 190


Asn Phe Asp Val Glu Gly Asp Asp Asp Val Ser Leu Trp Ser Tyr
        195                 200                 205


<210>  58
<211>  908
<212>  DNA
<213>  Arabidopsis thaliana


<220>
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<223>  n is a, c, g, or t

<220>
<223> CBF3  G42

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gacagagatc ttttagttac cttatccagt ttcttgaaac agagtactct tctgatcaat     120

gaactcattt tctgcttttt ctgaaatgtt tggctccgat tacgagtctt cggtttcctc     180

aggcggtgat tatattccga cgcttgcgag cagctgcccc aagaaaccgg cgggtcgtaa     240
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gaagtttcgt gagactcgtc acccaatata cagaggagtt cgtcggagaa actccggtaa      300

gtgggtttgt gaggttagag aaccaaacaa gaaaacaagg atttggctcg gaacatttca      360

aaccgctgag atggcagctc gagctcacga cgttgccgct ttagcccttc gtggccgatc      420

agcctgtctc aatttcgctg actcggcttg gagactccga atcccggaat caacttgcgc      480

taaggacatc caaaaggcgg cggctgaagc tgcgttggcg tttcaggatg agatgtgtga      540

tgcgacgacg gatcatggct tcgacatgga ggagacgttg gtggaggcta tttacacggc      600

ggaacagagc gaaaatgcgt tttatatgca cgatgaggcg atgtttgaga tgccgagttt      660

gttggctaat atggcagaag ggatgctttt gccgcttccg tccgtacagt ggaatcataa      720

tcatgaagtc gacggcgatg atgacgacgt atcgttatgg agttattaaa actcagatta      780

ttatttccat ttttagtacg atacttttta ttttattatt atttttagat ccttttttag      840

aatggaatct ncattatgtt tgtaaaactg agaaacgagt gtaaattaaa ttgattcagt      900

ttcagtat                                                               908


<210>  59
<211>  216
<212>  PRT
<213>  Arabidopsis thaliana

<220>
<223> CBF3 polypeptide G42

<400>  59

Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
1               5                   10                  15


Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
            20                  25                  30


Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
        35                  40                  45


Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
    50                  55                  60


Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
65                  70                  75                  80


Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
                85                  90                  95


Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
            100                 105                 110
```

Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
115 120 125

Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr
130 135 140

Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr
145 150 155 160

Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
165 170 175

Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
180 185 190

Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp
195 200 205

Asp Asp Val Ser Leu Trp Ser Tyr
210 215

<210> 60
<211> 632
<212> DNA
<213> Brassica napus

<220>
<223> bnCBF1

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gaaccaaaca agaaatctag aatttggctt ggaactttca aaacagctga gatggcagct 120

cgtgctcacg acgtcgctgc cctagccctc cgtggaagag gcgcctgcct caattatgcg 180

gactcggctt ggcggctccg catcccggag acaacctgcc acaaggatat ccagaaggct 240

gctgctgaag ccgcattggc ttttgaggct gagaaaagtg atgtgacgat gcaaaatggc 300

cagaacatgg aggagacgac ggcggtggct tctcaggctg aagtgaatga cacgacgaca 360

gaacatggca tgaacatgga ggaggcaacg gcagtggctt ctcaggctga ggtgaatgac 420

acgacgacgg atcatggcgt agacatggag gagacaatgg tggaggctgt ttttactggg 480

gaacaaagtg aagggtttaa catggcgaag gagtcgacgg tggaggctgc tgttgttacg 540

gaggaaccga gcaaaggatc ttacatggac gaggagtgga tgctcgagat gccgaccttg 600

ttggctgata tggcagaagg gatgctcctg cc 632

<210> 61
<211> 208
<212> PRT

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<213>  Brassica napus

<220>
<223> bnCBF1 polypeptide

<400>  61

His Pro Ile Tyr Arg Gly Val Arg Leu Arg Lys Ser Gly Lys Trp Val
1               5                   10                  15


Cys Glu Val Arg Glu Pro Asn Lys Lys Ser Arg Ile Trp Leu Gly Thr
            20                  25                  30


Phe Lys Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu
        35                  40                  45


Ala Leu Arg Gly Arg Gly Ala Cys Leu Asn Tyr Ala Asp Ser Ala Trp
    50                  55                  60


Arg Leu Arg Ile Pro Glu Thr Thr Cys His Lys Asp Ile Gln Lys Ala
65                  70                  75                  80


Ala Ala Glu Ala Ala Leu Ala Phe Glu Ala Glu Lys Ser Asp Val Thr
                85                  90                  95


Met Gln Asn Gly Gln Asn Met Glu Glu Thr Thr Ala Val Ala Ser Gln
            100                 105                 110


Ala Glu Val Asn Asp Thr Thr Thr Glu His Gly Met Asn Met Glu Glu
        115                 120                 125


Ala Thr Ala Val Ala Ser Gln Ala Glu Val Asn Asp Thr Thr Thr Asp
    130                 135                 140


His Gly Val Asp Met Glu Glu Thr Met Val Glu Ala Val Phe Thr Gly
145                 150                 155                 160


Glu Gln Ser Glu Gly Phe Asn Met Ala Lys Glu Ser Thr Val Glu Ala
                165                 170                 175


Ala Val Val Thr Glu Glu Pro Ser Lys Gly Ser Tyr Met Asp Glu Glu
            180                 185                 190


Trp Met Leu Glu Met Pro Thr Leu Leu Ala Asp Met Ala Glu Gly Met
        195                 200                 205


<210>  62
<211>  20
<212>  DNA
<213>  artificial sequence
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<220>
<223>  Artificial sequence


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<222>  (6)..(6)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (15)..(15)
<223>  n is a, c, g, or t

<220>
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<222>  (18)..(18)
<223>  n is a, c, g, or t

<220>
<223> Mol 368 reverse primer

<400>  62
cayccnatht aymgnggngt                                                  20


<210>  63
<211>  21
<212>  DNA
<213>  artificial sequence

<220>
<223>  Artificial sequence


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<222>  (3)..(3)
<223>  n is a, c, g, or t

<220>
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<222>  (6)..(6)
<223>  n is a, c, g, or t

<220>
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<222>  (12)..(12)
<223>  n is a, c, g, or t

<220>
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<223>  n is a, c, g, or t

<220>
<223> Mol 378 forward primer

<400>  63
ggnarnarca tnccytcngc c                                                21
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<210>  64
<211>  22
<212>  PRT
<213>  Arabidopsis thaliana

<220>
<223> DML motif of G867

<400>  64

His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Asn
1               5                   10                  15


Glu Glu Leu Glu Gln Ser
            20
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